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SEARCH REQUEST FORM

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****

Please provide a detailed statement of the search topic, and describe as specifically as possible the subject matter to be searched. Include the elected species or structures, keywords, synonyms, acronyms, and registry numbers, and combine with the concept or utility of the invention. Define any terms that may have a special meaning. Give examples or relevant citations, authors, etc, if known. Please attach a copy of the cover sheet, pertinent claims, and abstract.

Title of Invention: _____

Inventors (please provide full names): _____

_____

Earliest Priority Filing Date: _____

**For Sequence Searches Only* Please include all pertinent information (parent, child, divisional, or issued patent numbers) along with the appropriate serial number.*

****

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Searcher: D. Schreiber
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Searcher Location: Remsen EO1 A61
Date Searcher Picked Up: _____
Date Completed: 5/28/04
Searcher Prep & Review Time: 12
Clerical Prep Time: _____
Online Time: 27

Type of Search

NA Sequence (#)_____
AA Sequence (#) 2
Structure (#) _____
Bibliographic _____
Litigation _____
Fulltext _____
Patent Family _____
Other _____

Vendors and cost where applicable

STN _____
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Questel/Orbit _____
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Lexis/Nexis _____
Sequence Systems Compugen GCG
WWW/Internet _____
Other (specify) _____

PTO-1590 (8-01)

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: May 26, 2004, 09:24:28 ; Search time 18 Seconds
(without alignments)
1232.327 Million cell updates/sec

Title: US-09-966-781A-1
Perfect score: 2243
Sequence: 1 DQTALYIRMLGDVRVRSRAG.....DTDAAFELNSQLLPQENRLS 426

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_42:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	2243	100.0	482	1	CN7A_HUMAN	Q13946 homo sapien
2	2116	94.3	426	1	CN7A_RAT	O08593 rattus norv
3	2105	93.8	456	1	CN7A_MOUSE	P70453 mus musculu
4	1403.5	62.6	450	1	CN7B_HUMAN	Q9np56 homo sapien
5	1391.5	62.0	446	1	CN7B_MOUSE	Q9qxq1 mus musculu
6	555	24.7	844	1	CN4A_RAT	P54748 rattus norv
7	551	24.6	844	1	CN4A_MOUSE	O89084 mus musculu
8	550	24.5	721	1	CN4B_RAT	P14646 rattus norv
9	550	24.5	736	1	CN4B_HUMAN	Q07343 homo sapien
10	545	24.3	712	1	CN4C_HUMAN	Q08493 homo sapien
11	542	24.2	809	1	CN4D_HUMAN	Q08499 homo sapien
12	541	24.1	886	1	CN4A_HUMAN	P27815 homo sapien
13	539	24.0	672	1	CN4D_RAT	P14270 rattus norv
14	534.5	23.8	536	1	CN4C_RAT	P14644 rattus norv
15	503	22.4	829	1	CN8A_HUMAN	O60658 homo sapien
16	498.5	22.2	823	1	CN8A_MOUSE	O88502 mus musculu
17	493.5	22.0	549	1	YST1_CAEEL	Q22000 caenorhabdi
18	482	21.5	664	1	YFGK_CAEEL	O18696 caenorhabdi
19	478.5	21.3	777	1	CNA1_DROME	P12252 drosophila
20	471.5	21.0	793	1	REGA_DICDI	Q23917 dictyosteli
21	471.5	21.0	885	1	CN8B_HUMAN	O95263 homo sapien
22	470.5	21.0	534	1	CN1B_BOVIN	Q01061 bos taurus
23	470.5	21.0	535	1	CN1B_MOUSE	Q01065 mus musculu
24	469.5	20.9	535	1	CN1B_RAT	Q01066 rattus norv
25	466	20.8	654	1	CN1C_MOUSE	Q64338 mus musculu
26	461	20.6	768	1	CN1C_RAT	Q63421 rattus norv
27	457.5	20.4	536	1	CN1B_HUMAN	Q01064 homo sapien
28	456.5	20.4	565	1	CN1A_MOUSE	Q61481 mus musculu
29	452	20.2	534	1	CN1A_HUMAN	P54750 homo sapien
30	452	20.2	709	1	CN1C_HUMAN	Q14123 homo sapien
31	439.5	19.6	529	1	CN1A_BOVIN	P14100 bos taurus
32	418	18.6	534	1	CN9A_MOUSE	O70628 mus musculu
33	412	18.4	593	1	CN9A_HUMAN	O76083 homo sapien
34	402.5	17.9	1112	1	CN3B_HUMAN	Q13370 homo sapien
35	385.5	17.2	1108	1	CN3B_RAT	Q63085 rattus norv
36	385	17.2	799	1	CN3B_MOUSE	Q61409 mus musculu
37	375	16.7	1141	1	CN3A_HUMAN	Q14432 homo sapien
38	363	16.2	1141	1	CN3A_RAT	Q62865 rattus norv
39	348.5	15.5	865	1	CN5A_CANFA	O77746 canis famil
40	347.5	15.5	875	1	CN5A_HUMAN	O76074 homo sapien
41	336.5	15.0	833	1	CN5A_RAT	O54735 rattus norv
42	336.5	15.0	865	1	CN5A_MOUSE	Q8cg03 mus musculu
43	332.5	14.8	865	1	CN5A_BOVIN	Q28156 bos taurus
44	327	14.6	921	1	CN2A_BOVIN	P14099 bos taurus
45	323	14.4	928	1	CN2A_RAT	Q01062 rattus norv

ALIGNMENTS

```
RESULT 1
CN7A_HUMAN
ID   CN7A_HUMAN     STANDARD;      PRT;   482 AA.
AC   Q13946; O15380;
DT   15-JUL-1998 (Rel. 36, Created)
DT   15-JUL-1998 (Rel. 36, Last sequence update)
DT   15-MAR-2004 (Rel. 43, Last annotation update)
DE   High-affinity cAMP-specific 3',5'-cyclic phosphodiesterase 7A
DE   (EC 3.1.4.17) (HCP1) (TM22).
GN   PDE7A.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A. (ISOFORM PDE7A1).
RX   MEDLINE=93286141; PubMed=8389765;
RA   Michaeli T., Bloom T.J., Martins T., Loughney K., Ferguson K.,
RA   Riggs M., Rodgers L., Beavo J.A., Wigler M.;
RT   "Isolation and characterization of a previously undetected human cAMP
RT   phosphodiesterase by complementation of cAMP phosphodiesterase-
RT   deficient Saccharomyces cerevisiae.";
RL   J. Biol. Chem. 268:12925-12932(1993).
RN   [2]
RP   SEQUENCE FROM N.A. (ISOFORM PDE7A2).
RC   TISSUE=Skeletal muscle;
RX   MEDLINE=97341143; PubMed=9195912;
RA   Han P., Zhu X., Michaeli T.;
RT   "Alternative splicing of the high affinity cAMP-specific
RT   phosphodiesterase (PDE7A) mRNA in human skeletal muscle and heart.";
RL   J. Biol. Chem. 272:16152-16157(1997).
CC   -!- FUNCTION: Plays a role in signal transduction by regulating the
CC       intracellular concentration of cyclic nucleotides. This
CC       phosphodiesterase is highly specific for cAMP and may have a role
CC       in muscle signal transduction.
CC   -!- CATALYTIC ACTIVITY: Adenosine 3',5'-cyclic phosphate + H(2)O =
CC       adenosine 5'-phosphate.
CC   -!- COFACTOR: Requires divalent cations.
CC   -!- ENZYME REGULATION: Insensitive to all selective PDE inhibitors.
CC   -!- PATHWAY: Cyclic nucleotide metabolism.
CC   -!- SUBCELLULAR LOCATION: PDE7A1 (57 KDA) IS LOCATED MOSTLY TO SOLUBLE
CC       CELLULAR FRACTIONS. PDE7A2 (50 KDA) IS LOCATED TO PARTICULATE
CC       CELLULAR FRACTIONS.
CC   -!- ALTERNATIVE PRODUCTS:
CC       Event=Alternative splicing; Named isoforms=2;
CC       Name=PDE7A1;
CC         IsoId=Q13946-1; Sequence=Displayed;
CC       Name=PDE7A2;
CC         IsoId=Q13946-2; Sequence=VSP_004593;
CC   -!- TISSUE SPECIFICITY: PDE7A1 is found at high levels in skeletal
CC       muscle and at low levels in a variety of tissues including brain
CC       and heart. It is expressed as well in two T-cell lines. PDE7A2 is
CC       found abundantly in skeletal muscle and at low levels in heart.
CC   -!- DEVELOPMENTAL STAGE: Developmentally regulated. PDE7A1 and PDE7A2
CC       are found in several fetal tissues, expression is reduced
CC       throughout development. It persists strongly only in adult
```

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CC       skeletal muscle.
CC   -!- DOMAIN: Composed of a C-terminal catalytic domain containing two
CC       putative divalent metal sites and an N-terminal regulatory domain.
CC   -!- SIMILARITY: Belongs to the cyclic nucleotide phosphodiesterase
CC       family.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; L12052; AAA35644.2; -.
DR   EMBL; U67932; AAB65772.1; -.
DR   Genew; HGNC:8791; PDE7A.
DR   MIM; 171885; -.
DR   GO; GO:0000267; C:cell fraction; NAS.
DR   GO; GO:0004115; F:cAMP-specific phosphodiesterase activity; TAS.
DR   GO; GO:0007165; P:signal transduction; NAS.
DR   InterPro; IPR003607; Met_phsphohydro.
DR   InterPro; IPR002073; PDEase.
DR   Pfam; PF00233; PDEase; 1.
DR   PRINTS; PR00387; PDIESTERASE1.
DR   SMART; SM00471; HDc; 1.
DR   PROSITE; PS00126; PDEASE_I; 1.
KW   Hydrolase; cAMP; Phosphorylation; Alternative splicing.
FT   DOMAIN       28     33       POLY-SER.
FT   DOMAIN      187    451       CATALYTIC (BY SIMILARITY).
FT   MOD_RES      84     84       PHOSPHORYLATION (POTENTIAL).
FT   VARSPLIC      1     46       MEVCYQLPVLPLDRPVPQHVLSRRGAISFSSSSALFGCPNP
FT                                RQLSQ -> MGITLIWCLALVLIKWITSK (in isoform
FT                                PDE7A2).
FT                                /FTId=VSP_004593.
SQ   SEQUENCE   482 AA;  55505 MW;  3B3C8F6E9154F88C CRC64;

  Query Match             100.0%;  Score 2243;  DB 1;  Length 482;
  Best Local Similarity   100.0%;  Pred. No. 1.4e-176;
  Matches  426;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 DQTALYIRMLGDVRVRSRAGFESERRGSHPYIDFRIFHSQSEIEVSVSARNIRRLLSFQR 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         57 DQTALYIRMLGDVRVRSRAGFESERRGSHPYIDFRIFHSQSEIEVSVSARNIRRLLSFQR 116

Qy         61 YLRSSRFFRGTAVSNSLNILDDDYNGQAKCMLEKVGNWNFDIFLFDRLTNGNSLVSLTFH 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        117 YLRSSRFFRGTAVSNSLNILDDDYNGQAKCMLEKVGNWNFDIFLFDRLTNGNSLVSLTFH 176

Qy        121 LFSLHGLIEYFHLDMMKLRRFLVMIQEDYHSQNPYHNAVHAADVTQAMHCYLKEPKLANS 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        177 LFSLHGLIEYFHLDMMKLRRFLVMIQEDYHSQNPYHNAVHAADVTQAMHCYLKEPKLANS 236

Qy        181 VTPWDILLSLIAAATHDLDHPGVNQPFLIKTNHYLATLYKNTSVLENHHWRSAVGLLRES 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        237 VTPWDILLSLIAAATHDLDHPGVNQPFLIKTNHYLATLYKNTSVLENHHWRSAVGLLRES 296

Qy        241 GLFSHLPLESRQQMETQIGALILATDISRQNEYLSLFRSHLDRGDLCLEDTRHRHLVLQM 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        297 GLFSHLPLESRQQMETQIGALILATDISRQNEYLSLFRSHLDRGDLCLEDTRHRHLVLQM 356

Qy        301 ALKCADICNPCRTWELSKQWSEKVTEEFFHQGDIEKKYHLGVSPLCDRHTESIANIQIGF 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        357 ALKCADICNPCRTWELSKQWSEKVTEEFFHQGDIEKKYHLGVSPLCDRHTESIANIQIGF 416

Qy        361 MTYLVEPLFTEWARFSNTRLSQTMLGHVGLNKASWKGLQREQSSSEDTDAAFELNSQLLP 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        417 MTYLVEPLFTEWARFSNTRLSQTMLGHVGLNKASWKGLQREQSSSEDTDAAFELNSQLLP 476

Qy        421 QENRLS 426
              ||||||
Db        477 QENRLS 482
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RESULT 2
CN7A_RAT
ID   CN7A_RAT       STANDARD;      PRT;   426 AA.
AC   O08593;
DT   15-JUL-1998 (Rel. 36, Created)
DT   15-JUL-1998 (Rel. 36, Last sequence update)
DT   28-FEB-2003 (Rel. 41, Last annotation update)
DE   High-affinity cAMP-specific 3',5'-cyclic phosphodiesterase 7A
DE   (EC 3.1.4.17) (Rolipram-insensitive phosphodiesterase type 7)
DE   (Fragment).
GN   PDE7A.
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Brain;
RX   MEDLINE=98176136; PubMed=9515162;
RA   Hoffmann R., Abdel'Al S., Engels P.;
RT   "Differential distribution of rat PDE-7 mRNA in embryonic and adult
RT   rat brain.";
RL   Cell Biochem. Biophys. 28:103-113(1998).
CC   -!- FUNCTION: Plays a role in signal transduction by regulating the
CC       intracellular concentration of cyclic nucleotides. This
CC       phosphodiesterase is highly specific for cAMP and may have a role
CC       in muscle signal transduction (By similarity).
CC   -!- CATALYTIC ACTIVITY: Adenosine 3',5'-cyclic phosphate + H(2)O =
CC       adenosine 5'-phosphate.
CC   -!- COFACTOR: Requires divalent cations (By similarity).
CC   -!- ENZYME REGULATION: Insensitive to all selective PDE inhibitors (By
CC       similarity).
CC   -!- PATHWAY: Cyclic nucleotide metabolism.
CC   -!- DOMAIN: Composed of a C-terminal catalytic domain containing two
CC       putative divalent metal sites and an N-terminal regulatory domain.
CC   -!- SIMILARITY: Belongs to the cyclic nucleotide phosphodiesterase
CC       family.
CC   ---------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; U77880; AAB51234.1; -.
DR   InterPro; IPR003607; Met_phsphohydro.
DR   InterPro; IPR002073; PDEase.
DR   Pfam; PF00233; PDEase; 1.
DR   PRINTS; PR00387; PDIESTERASE1.
DR   SMART; SM00471; HDc; 1.
DR   PROSITE; PS00126; PDEASE_I; 1.
KW   Hydrolase; cAMP.
FT   NON_TER       1      1
FT   DOMAIN      131    395       CATALYTIC (BY SIMILARITY).
SQ   SEQUENCE   426 AA;  49274 MW;  129BDC01C9351D26 CRC64;

  Query Match             94.3%;  Score 2116;  DB 1;  Length 426;
  Best Local Similarity   94.1%;  Pred. No. 3.2e-166;
  Matches  401;  Conservative    9;  Mismatches   16;  Indels    0;  Gaps    0;

Qy          1 DQTALYIRMLGDVRVRSRAGFESERRGSHPYIDFRIFHSQSEIEVSVSARNIRRLLSFQR 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 DQTALYIRMLGDVRVRSRAGFETERRGSHPYIDFRIFHAQSEIEASVSARNIRRLLSFQR 60

Qy         61 YLRSSRFFRGTAVSNSLNILDDDYNGQAKCMLEKVGNWNFDIFLFDRLTNGNSLVSLTFH 120
              ||||||||||  |  ||||||:||||||||||||||||||||||||||||||||||||||
Db         61 YLRSSRFFRGATVCRSLNILDEDYNGQAKCMLEKVGNWNFDIFLFDRLTNGNSLVSLTFH 120

Qy        121 LFSLHGLIEYFHLDMMKLRRFLVMIQEDYHSQNPYHNAVHAADVTQAMHCYLKEPKLAN  80
              ||||||||||||||:||||||||||||||||||||||||||||||||||||||||||||
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Db        121 LFSLHGLIEYFHLDMVKLRRFLVMIQEDYHSQNPYHNAVHAADVTQAMHCYLKEPKLANS 180

Qy        181 VTPWDILLSLIAAATHDLDHPGVNQPFLIKTNHYLATLYKNTSVLENHHWRSAVGLLRES 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 VTPWDILLSLIAAATHDLDHPGVNQPFLIKTNHYLATLYKNTSVLENHHWRSAVGLLRES 240

Qy        241 GLFSHLPLESRQQMETQIGALILATDISRQNEYLSLFRSHLDRGDLCLEDTRHRHLVLQM 300
              |||||||||| :|| |||||||||||||||||||||||:||| |:| |||||||||
Db        241 GLFSHLPLESRHEMEAQIGALILATDISRQNEYLSLFRSHLDKGDLHLDDGRHRHLVLQM 300

Qy        301 ALKCADICNPCRTWELSKQWSEKVTEEFFHQGDIEKKYHLGVSPLCDRHTESIANIQIGF 360
              |||||||||||| |||||||||||||||||||||||||||||||| ||||||||||
Db        301 ALKCADICNPCRNWELSKQWSEKVTEEFFHQGDIEKKYHLGVSPLCDRQTESIANIQIGF 360

Qy        361 MTYLVEPLFTEWARFSNTRLSQTMLGHVGLNKASWKGLQREQSSSEDTDAAFELNSQLLP 420
              |||| ||||||||||:|||||||||||||||||||:| |||| ||||||||||
Db        361 MTYLQEPLFTEWARFSDTRLSQTMLGHVGLNKASWKGLQRQQPSSEDASAAFELNSQLLT 420

Qy        421 QENRLS 426
              ||||||
Db        421 QENRLS 426
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RESULT 3
CN7A_MOUSE
ID   CN7A_MOUSE     STANDARD;      PRT;   456 AA.
AC   P70453; Q9ERB3;
DT   15-JUL-1998 (Rel. 36, Created)
DT   15-JUL-1998 (Rel. 36, Last sequence update)
DT   15-MAR-2004 (Rel. 43, Last annotation update)
DE   High-affinity cAMP-specific 3',5'-cyclic phosphodiesterase 7A
DE   (EC 3.1.4.17) (P2A).
GN   PDE7A.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A. (ISOFORM 1).
RC   TISSUE=Skeletal muscle;
RX   MEDLINE=97098542; PubMed=8943082;
RA   Bloom T.J., Beavo J.A.;
RT   "Identification and tissue-specific expression of PDE7
RT   phosphodiesterase splice variants.";
RL   Proc. Natl. Acad. Sci. U.S.A. 93:14188-14192(1996).
RN   [2]
RP   SEQUENCE FROM N.A. (ISOFORM 2).
RC   TISSUE=Brain, and Testis;
RX   MEDLINE=20483661; PubMed=11027622;
RA   Wang P., Wu P., Egan R.W., Billah M.M.;
RT   "Cloning, characterization, and tissue distribution of mouse
RT   phosphodiesterase 7A1.";
RL   Biochem. Biophys. Res. Commun. 276:1271-1277(2000).
CC   -!- FUNCTION: Plays a role in signal transduction by regulating the
CC       intracellular concentration of cyclic nucleotides. This
CC       phosphodiesterase is highly specific for cAMP and may have a role
CC       in muscle signal transduction.
CC   -!- CATALYTIC ACTIVITY: Adenosine 3',5'-cyclic phosphate + H(2)O =
CC       adenosine 5'-phosphate.
CC   -!- COFACTOR: Requires divalent cations.
CC   -!- ENZYME REGULATION: Insensitive to all selective PDE inhibitors.
CC   -!- PATHWAY: Cyclic nucleotide metabolism.
CC   -!- ALTERNATIVE PRODUCTS:
CC       Event=Alternative splicing; Named isoforms=2;
CC         Comment=Additional isoforms seem to exist;
CC       Name=1; Synonyms=PDE7A2;
CC         IsoId=P70453-1; Sequence=Displayed;
CC       Name=2; Synonyms=PDE7A1;
CC         IsoId=P70453-2; Sequence=VSP_004594;
CC   -!- TISSUE SPECIFICITY: Widely expressed with highest levels in the
CC       skeletal muscle.
CC   -!- DOMAIN: Composed of a C-terminal catalytic domain containing two
CC       putative divalent metal sites and an N-terminal regulatory domain.
CC   -!- SIMILARITY: Belongs to the cyclic nucleotide phosphodiesterase
CC       family.
CC   ---------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; U68171; AAB08479.1; -.
DR   EMBL; AY007702; AAG16295.1; -.
DR   MGD; MGI:1202402; Pde7a.
DR   InterPro; IPR003607; Met_phsphohydro.
DR   InterPro; IPR002073; PDEase.
DR   Pfam; PF00233; PDEase; 1.
DR   PRINTS; PR00387; PDIESTERASE1.
DR   SMART; SM00471; HDc; 1.
DR   PROSITE; PS00126; PDEASE_I; 1.
KW   Hydrolase; cAMP; Alternative splicing.
FT   DOMAIN      161     425       CATALYTIC (BY SIMILARITY).
FT   VARSPLIC      1      20       MGITLIWCLALVLIKWITSK -> MEVCYQLPVLPLDRPVP
FT                                 QHVLSRRGAISFSSSSALFGCPHPRQLSQ (in isoform
FT                                 2).
FT                                 /FTId=VSP_004594.
FT   CONFLICT    407     407       A -> D (IN REF. 2).
SQ   SEQUENCE   456 AA;  52441 MW;  0B826B96490D9F6E CRC64;

  Query Match             93.8%;  Score 2105;  DB 1;  Length 456;
  Best Local Similarity   93.7%;  Pred. No. 2.8e-165;
  Matches  399;  Conservative   13;  Mismatches   14;  Indels    0;  Gaps    0;

Qy          1 DQTALYIRMLGDVRVRSRAGFESERRGSHPYIDFRIFHSQSEIEVSVSARNIRRLLSFQR 60
              |||||||||||||||||||:||||||||||||||||:|| ||||||||||||||
Db         31 DQTALYIRMLGDVRVRSRAGFETERRGSHPYIDFRIFHSQSDIEASVSARNIRRLLSFQR 90

Qy         61 YLRSSRFFRGTAVSNSLNILDDDYNGQAKCMLEKVGNWNFDIFLFDRLTNGNSLVSLTFH 120
              |||||| ||| | :||:|||:|||||||||||||||||||||||||||||||||||||
Db         91 YLRSSRVFRGATVCSSLDILDEDYNGQAKCMLEKVGNWNFDIFLFDRLTNGNSLVSLTFH 150

Qy        121 LFSLHGLIEYFHLDMMKLRRFLVMIQEDYHSQNPYHNAVHAADVTQAMHCYLKEPKLANS 180
              |||||||||||||:|||||||||||||||||||||||||||||||||||||||||:|
Db        151 LFSLHGLIEYFHLDMVKLRRFLVMIQEDYHSQNPYHNAVHAADVTQAMHCYLKEPKLASS 210

Qy        181 VTPWDILLSLIAAATHDLDHPGVNQPFLIKTNHYLATLYKNTSVLENHHWRSAVGLLRES 240
              ||||||||||||||||||||||||||||||||||||||:|||||||||||||||
Db        211 VTPWDILLSLIAAATHDLDHPGVNQPFLIKTNHYLATLYKNSSVLENHHWRSAVGLLRES 270

Qy        241 GLFSHLPLESRQQMETQIGALILATDISRQNEYLSLFRSHLDRGDLCLEDTRHRHLVLQM 300
              |||||||||||:|| |||||||||||||||||||||||:||| |:| |||||||||
Db        271 GLFSHLPLESRQEMEAQIGALILATDISRQNEYLSLFRSHLDKGDLHLDDGRHRHLVLQM 330

Qy        301 ALKCADICNPCRTWELSKQWSEKVTEEFFHQGDIEKKYHLGVSPLCDRHTESIANIQIGF 360
              |||||||||||| |||||||||||||||||||||||||||||||| ||||||||||
Db        331 ALKCADICNPCRNWELSKQWSEKVTEEFFHQGDIEKKYHLGVSPLCDRQTESIANIQIGF 390

Qy        361 MTYLVEPLFTEWARFSNTRLSQTMLGHVGLNKASWKGLQREQSSSEDTDAAFELNSQLLP 420
              |||||||||||||| ||||||||||||||||||||||:| |||| :||||||||||
Db        391 MTYLVEPLFTEWARFSATRLSQTMLGHVGLNKASWKGLQRQQPSSEDANAAFELNSQLLT 450

Qy        421 QENRLS 426
              ||||||
Db        451 QENRLS 456
```

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RESULT 4
CN7B_HUMAN
ID   CN7B_HUMAN     STANDARD;      PRT;   450 AA.
AC   Q9NP56;
DT   16-OCT-2001 (Rel. 40, Created)
DT   16-OCT-2001 (Rel. 40, Last sequence update)
DT   15-MAR-2004 (Rel. 43, Last annotation update)
```

```
DE   cAMP-specific 3',5'-cyclic phosphodiesterase 7B (EC 3.1.4.17).
GN   PDE7B.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Brain;
RX   MEDLINE=20275458; PubMed=10814504;
RA   Sasaki T., Kotera J., Yuasa K., Omori K.;
RT   "Identification of human PDE7B, a cAMP-specific phosphodiesterase.";
RL   Biochem. Biophys. Res. Commun. 271:575-583(2000).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Fetal brain;
RX   MEDLINE=20329226; PubMed=10872825;
RA   Gardner C.E., Robas N.M., Cawkill D., Fidock M.D.;
RT   "Cloning and characterisation of the human and mouse PDE7B, a novel
RT   cAMP-specific nucleotide phosphodiesterase.";
RL   Biochem. Biophys. Res. Commun. 272:186-192(2000).
CC   -!- FUNCTION: May be involved in the control of cAMP-mediated neural
CC       activity and cAMP metabolism in the brain.
CC   -!- CATALYTIC ACTIVITY: Adenosine 3',5'-cyclic phosphate + H(2)O =
CC       adenosine 5'-phosphate.
CC   -!- COFACTOR: Requires divalent cations (By similarity).
CC   -!- ENZYME REGULATION: Inhibited by dipyridamole, IBMX and SCH51866.
CC       Insensitive to zaprinast, rolipram, and milrinone.
CC   -!- PATHWAY: Cyclic nucleotide metabolism.
CC   -!- TISSUE SPECIFICITY: Highly expressed in brain. Also expressed in
CC       heart, liver, skeletal muscle and pancreas.
CC   -!- DOMAIN: Composed of a C-terminal catalytic domain containing two
CC       putative divalent metal sites and an N-terminal regulatory domain.
CC   -!- SIMILARITY: Belongs to the cyclic nucleotide phosphodiesterase
CC       family.
CC   ---------------------------------------------------------------------
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CC   use by non-profit institutions as long as its content is in no way
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; AB038040; BAA96537.1; -.
DR   EMBL; AJ251860; CAB92441.1; -.
DR   PIR; JC7266; JC7266.
DR   PDB; 1LXW; 26-JUN-02.
DR   Genew; HGNC:8792; PDE7B.
DR   MIM; 604645; -.
DR   GO; GO:0004115; F:cAMP-specific phosphodiesterase activity; TAS.
DR   GO; GO:0007165; P:signal transduction; TAS.
DR   GO; GO:0007268; P:synaptic transmission; TAS.
DR   InterPro; IPR003607; Met_phsphohydro.
DR   InterPro; IPR002073; PDEase.
DR   Pfam; PF00233; PDEase; 1.
DR   PRINTS; PR00387; PDIESTERASE1.
DR   SMART; SM00471; HDc; 1.
DR   PROSITE; PS00126; PDEASE_I; 1.
KW   Hydrolase; cAMP; 3D-structure.
FT   DOMAIN      172     410       CATALYTIC (BY SIMILARITY).
SQ   SEQUENCE   450 AA;  51835 MW;  EC142BF3E28D0028 CRC64;

  Query Match             62.6%;  Score 1403.5;  DB 1;  Length 450;
  Best Local Similarity   62.6%;  Pred. No. 1e-107;
  Matches  258;  Conservative   66;  Mismatches   87;  Indels    1;  Gaps    1;

Qy          1 DQTALYIRMLGDVRVRSRAGFESERRGSHPYIDFRIFHSQSEIEVSVSARNIRRLLSFQR 60
              ||  |  : ||||:|:| : |  :|||||:|:||||: :| :      : : ::|||||||
Db         18 DQNAKCVCMLGDIRLRGQTGVRAERRGSYPFIDFRLLNSTTYSGEIGTKKKVKRLLSFQR 77

Qy         61 YLRSSRFFRGTAVSNSLNILDDDYNGQAKCMLEKVGNWNFDIFLFDRLTNGNSLVSLTFH 120
                 |  :||  ||       |::||:|| |||: || ||| |:|||||||||||||||:|  |

Db         78 YFHASRLLRGIIPQAPLHLLDEDYLGQARHMLSKVGMWDFDIFLFDRLTNGNSLVTLLCH 137

Qy        121 LFSLHGLIEYFHLDMMKLRRFLVMIQEDYHSQNPYHNAVHAADVTQAMHCYLKEPKLANS 180
              ||: |||| :| |||: | |||||:|||||||||||||||||||||||||||||||:
Db        138 LFNTHGLIHHFKLDMVTLHRFLVMVQEDYHSQNPYHNAVHAADVTQAMHCYLKEPKLASF 197

Qy        181 VTPWDILLSLIAAATHDLDHPGVNQPFLIKTNHYLATLYKNTSVLENHHWRSAVGLLRES 240
              :|| ||:| |:||| ||:|||||||||||||:|| ||:| |||||||||| :|:||||
Db        198 LTPLDIMLGLLAAAAHDVDHPGVNQPFLIKTNHHLANLYQNMSVLENHHWRSTIGMLRES 257

Qy        241 GLFSHLPLESRQQMETQIGALILATDISRQNEYLSLFRSHLDRGDLCLEDTRHRHLVLQM 300
              | :||| |  | :| |:|:||||||:||||:|:  ::||   || ||| : || :||:
Db        258 RLLAHLPKEMTQDIEQQLGSLILATDINRQNEFLTRLKAHLHNKDLRLEDAQDRHFMLQI 317

Qy        301 ALKCADICNPCRTWELSKQWSEKVTEEFFHQGDIEKKYHLGVSPLCDRHTESIANIQIGF 360
              |||||||||||| ||:|||||:| |||: ||::|:|: | :||||::  :|| :|||||
Db        318 ALKCADICNPCRIWEMSKQWSERVCEEFYRQGELEQKFELEISPLCNQQKDSIPSIQIGF 377

Qy        361 MTYLVEPLFTEWARFS-NTRLSQTMLGHVGLNKASWKGLQREQSSSEDTDAA 411
              |:|:|||| ||| |: |: ||: |||| :  ||| || |   | |  :  :
Db        378 MSYIVEPLFREWAHFTGNSTLSENMLGHLAHNKAQWKSLLPRQHRSRGSSGS 429


RESULT 5
CN7B_MOUSE
ID   CN7B_MOUSE     STANDARD;      PRT;   446 AA.
AC   Q9QXQ1;
DT   16-OCT-2001 (Rel. 40, Created)
DT   16-OCT-2001 (Rel. 40, Last sequence update)
DT   15-MAR-2004 (Rel. 43, Last annotation update)
DE   cAMP-specific 3',5'-cyclic phosphodiesterase 7B (EC 3.1.4.17).
GN   PDE7B.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=20087273; PubMed=10618442;
RA   Hetman J.M., Soderling S.H., Glavas N.A., Beavo J.A.;
RT   "Cloning and characterization of PDE7B, a cAMP-specific
RT   phosphodiesterase.";
RL   Proc. Natl. Acad. Sci. U.S.A. 97:472-476(2000).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J;
RX   MEDLINE=20329226; PubMed=10872825;
RA   Gardner C.E., Robas N.M., Cawkill D., Fidock M.D.;
RT   "Cloning and characterisation of the human and mouse PDE7B, a novel
RT   cAMP-specific nucleotide phosphodiesterase.";
RL   Biochem. Biophys. Res. Commun. 272:186-192(2000).
CC   -!- FUNCTION: May be involved in the control of cAMP-mediated neural
CC       activity and cAMP metabolism in the brain.
CC   -!- CATALYTIC ACTIVITY: Adenosine 3',5'-cyclic phosphate + H(2)O =
CC       adenosine 5'-phosphate.
CC   -!- COFACTOR: Requires divalent cations (By similarity).
CC   -!- ENZYME REGULATION: Inhibited by dipyridamole, IBMX and SCH51866.
CC       Insensitive to zaprinast, rolipram, and milrinone.
CC   -!- PATHWAY: Cyclic nucleotide metabolism.
CC   -!- TISSUE SPECIFICITY: Highly expressed in brain.
CC   -!- DOMAIN: Composed of a C-terminal catalytic domain containing two
CC       putative divalent metal sites and an N-terminal regulatory domain.
CC   -!- SIMILARITY: Belongs to the cyclic nucleotide phosphodiesterase
CC       family.
CC   ---------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
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DR   EMBL; AF190639; AAF25195.1; -.
DR   EMBL; AJ251859; CAB92530.1; -.
DR   MGD; MGI:1352752; Pde7b.
DR   GO; GO:0004115; F:cAMP-specific phosphodiesterase activity; IDA.
DR   InterPro; IPR003607; Met_phsphohydro.
DR   InterPro; IPR002073; PDEase.
DR   Pfam; PF00233; PDEase; 1.
DR   PRINTS; PR00387; PDIESTERASE1.
DR   SMART; SM00471; HDc; 1.
DR   PROSITE; PS00126; PDEASE_I; 1.
KW   Hydrolase; cAMP.
FT   DOMAIN      172    410       CATALYTIC (BY SIMILARITY).
SQ   SEQUENCE   446 AA;  51337 MW;  7C052664B693A5A8 CRC64;

  Query Match           62.0%;  Score 1391.5;  DB 1;  Length 446;
  Best Local Similarity  62.1%;  Pred. No. 1e-106;
  Matches  256;  Conservative   67;  Mismatches   84;  Indels    5;  Gaps    2;

Qy          1 DQTALYIRMLGDVRVRSRAGFESERRGSHPYIDFRIFHSQSEIEVSVSARNIRRLLSFQR 60
              :|:   : |||||:| : |  :|||||:|:||||: :: :      : : ::|||||||
Db         18 EQSVKCVCMLGDVRLRGQTGVPAERRGSYPFIDFRLLNNTTHSGEIGTKKKVKRLLSFQR 77

Qy         61 YLRSSRFFRGTAVSNSLNILDDDYNGQAKCMLEKVGNWNFDIFLFDRLTNGNSLVSLTFH 120
               |  :||  ||       |::||:|| |||: || ||| |:|||||||||||||||:|  |
Db         78 YFHASRLLRGIIPQAPLHLLDEDYLGQARHMLSKVGTWDFDIFLFDRLTNGNSLVTLLCH 137

Qy        121 LFSLHGLIEYFHLDMMKLRRFLVMIQEDYHSQNPYHNAVHAADVTQAMHCYLKEPKLANS 180
              ||: |||| :| ||| : | |||||:|||||  |||||||||||||||||||||||||:
Db        138 LFNSHGLIHHFKLDMVTLHRFLVMVQEDYHGHNPYHNAVHAADVTQAMHCYLKEPKLASF 197

Qy        181 VTPWDILLSLIAAATHDLDHPGVNQPFLIKTNHYLATLYKNTSVLENHHWRSAVGLLRES 240
              :|| ||:|  |:||| ||:|||||||||||||:|| ||:| |||||||||| :|:||||
Db        198 LTPLDIMLGLLAAAAHDVDHPGVNQPFLIKTNHHLANLYQNMSVLENHHWRSTIGMLRES 257

Qy        241 GLFSHLPLESRQQMETQIGALILATDISRQNEYLSLFRSHLDRGDLCLEDTRHRHLVLQM 300
               | :||| |  | :| |:|:|||||||:||||:|:  ::||   || ||: : || :||:
Db        258 RLLAHLPKEMTQDIEQQLGSLILATDINRQNEFLTRLKAHLHNKDLRLENVQDRHFMLQI 317

Qy        301 ALKCADICNPCRTWELSKQWSEKVTEEFFHQGDIEKKYHLGVSPLCDRHTESIANIQIGF 360
              |||||||||||| ||:|||||:| |||: |||:|:|: | :||||::  :|| :|||||
Db        318 ALKCADICNPCRIWEMSKQWSERVCEEFYRQGDLEQKFELEISPLCNQQKDSIPSIQIGF 377

Qy        361 MTYLVEPLFTEWARFS-NTRLSQTMLGHVGLNKASWKGL----QREQSSSED 407
              |||:||||| ||||||: |: ||: || |:  ||| || |      | : | :|
Db        378 MTYIVEPLFREWARFTGNSTLSENMLSHLAHNKAQWKSLLSNQHRRRGSGQD 429


RESULT 6
CN4A_RAT
ID   CN4A_RAT       STANDARD;      PRT;   844 AA.
AC   P54748; P14645;
DT   01-APR-1990 (Rel. 14, Created)
DT   01-OCT-1996 (Rel. 34, Last sequence update)
DT   10-OCT-2003 (Rel. 42, Last annotation update)
DE   cAMP-specific 3',5'-cyclic phosphodiesterase 4A (EC 3.1.4.17)
DE   (DPDE2).
GN   PDE4A.
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   SEQUENCE FROM N.A. (ISOFORMS 3; 4 AND 5).
RX   MEDLINE=89264472; PubMed=2542942;
RA   Davis R.L., Takayasu H., Eberwine M., Myres J.;
RT   "Cloning and characterization of mammalian homologs of the Drosophila
RT   dunce+ gene.";
RL   Proc. Natl. Acad. Sci. U.S.A. 86:3604-3608(1989).
RN   [2]
RP   SEQUENCE FROM N.A. (ISOFORMS 1; 3; 4 AND 5).
RC   TISSUE=Brain;
RX   MEDLINE=95047482; PubMed=7958996;
RA   Bolger G.B., Rodgers L., Riggs M.;
RT   "Differential CNS expression of alternative mRNA isoforms of the
RT   mammalian genes encoding cAMP-specific phosphodiesterases.";
RL   Gene 149:237-244(1994).
RN   [3]
RP   SEQUENCE FROM N.A. (ISOFORM 2).
RC   STRAIN=Sprague-Dawley; TISSUE=Testis;
RX   MEDLINE=96132847; PubMed=8557632;
RA   Bolger G.B., McPhee I., Houslay M.D.;
RT   "Alternative splicing of cAMP-specific phosphodiesterase mRNA
RT   transcripts. Characterization of a novel tissue-specific isoform,
RT   RNPDE4A8.";
RL   J. Biol. Chem. 271:1065-1071(1996).
RN   [4]
RP   SEQUENCE OF 319-677 FROM N.A. (ISOFORM 3/4).
RC   TISSUE=Testis;
RX   MEDLINE=89315790; PubMed=2546153;
RA   Swinnen J.V., Joseph D.R., Conti M.;
RT   "Molecular cloning of rat homologues of the Drosophila melanogaster
RT   dunce cAMP phosphodiesterase: evidence for a family of genes.";
RL   Proc. Natl. Acad. Sci. U.S.A. 86:5325-5329(1989).
RN   [5]
RP   STRUCTURE BY NMR OF 1-26 OF ISOFORM 3.
RX   MEDLINE=96279244; PubMed=8663181;
RA   Smith K.J., Scotland G., Beattie J., Trayer I.P., Houslay M.D.;
RT   "Determination of the structure of the N-terminal splice region of
RT   the cyclic AMP-specific phosphodiesterase RD1 (RNPDE4A1) by 1H NMR
RT   and identification of the membrane association domain using chimeric
RT   constructs.";
RL   J. Biol. Chem. 271:16703-16711(1996).
CC   -!- CATALYTIC ACTIVITY: Adenosine 3',5'-cyclic phosphate + H(2)O =
CC       adenosine 5'-phosphate.
CC   -!- ENZYME REGULATION: Inhibited by rolipram.
CC   -!- PATHWAY: Cyclic nucleotide metabolism.
CC   -!- ALTERNATIVE PRODUCTS:
CC       Event=Alternative splicing; Named isoforms=5;
CC       Name=1;
CC         IsoId=P54748-1; Sequence=Displayed;
CC       Name=2; Synonyms=PDE4A8;
CC         IsoId=P54748-2; Sequence=VSP_004565;
CC       Name=3;
CC         IsoId=P54748-3; Sequence=VSP_004566, VSP_004567;
CC       Name=4; Synonyms=Medium;
CC         IsoId=P54748-4; Sequence=VSP_004568;
CC       Name=5; Synonyms=Short;
CC         IsoId=P54748-5; Sequence=VSP_004569, VSP_004570;
CC   -!- TISSUE SPECIFICITY: Isoform 2 is testis specific.
CC   -!- SIMILARITY: Belongs to the cyclic nucleotide phosphodiesterase
CC       family.
CC   ---------------------------------------------------------------------
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CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; L27057; AAC27098.1; -.
DR   EMBL; L36467; AAB00357.1; -.
DR   EMBL; L27062; AAA56859.1; -.
DR   EMBL; M25348; AAA41848.1; -.
DR   EMBL; M28411; AAA41823.1; -.
DR   EMBL; M26715; AAC37699.1; -.
DR   EMBL; M26716; AAA41101.1; -.
DR   EMBL; M26717; AAA41102.1; -.
DR   PIR; I53865; I53865.
DR   PIR; I67946; I67946.
DR   PDB; 1LOI; 15-MAY-97.
DR   InterPro; IPR003607; Met_phsphohydro.
DR   InterPro; IPR002073; PDEase.
DR   Pfam; PF00233; PDEase; 1.
DR   PRINTS; PR00387; PDIESTERASE1.
DR   SMART; SM00471; HDc; 1.
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DR   PROSITE; PS00126; PDEASE_I; 1.
KW   Hydrolase; cAMP; Alternative splicing; Multigene family; 3D-structure.
FT   VARSPLIC      1    102       MEPPAAPSERSLSLSLPGPREGQATLKPPPQHLWRQPRTPI
FT                                RIQQRGYPDSAERSETERSPHRPIERADAVDTGDRPGLRTT
FT                                RMSWPSSFHGTGTGGGSSRR -> MPSRKRLTLPRIFIVRK
FT                                NGNS (in isoform 2).
FT                                /FTId=VSP_004565.
FT   VARSPLIC      1    234       Missing (in isoform 3).
FT                                /FTId=VSP_004566.
FT   VARSPLIC    235    256       WCLEQLETMQTYRSVSEMASHK -> MPLVDFFCETCSKPW
FT                                LVGWWDQ (in isoform 3).
FT                                /FTId=VSP_004567.
FT   VARSPLIC      1    259       Missing (in isoform 4).
FT                                /FTId=VSP_004568.
FT   VARSPLIC      1    318       Missing (in isoform 5).
FT                                /FTId=VSP_004569.
FT   VARSPLIC    354    386       Missing (in isoform 5).
FT                                /FTId=VSP_004570.
FT   CONFLICT    465    466       GV -> AL (IN REF. 4).
FT   CONFLICT    603    604       GD -> AH (IN REF. 4).
FT   CONFLICT    833    833       A -> T (IN REF. 1).
SQ   SEQUENCE   844 AA;  93438 MW;  1A5F5101E4DBF1B6 CRC64;

  Query Match             24.7%;  Score 555;  DB 1;  Length 844;
  Best Local Similarity   32.6%;  Pred. No. 1.1e-37;
  Matches  127;  Conservative   77;  Mismatches  154;  Indels   32;  Gaps    7;

Qy          8 RMLGDVRVRSRAGFESERRGSHPYIDFRIFHSQSEIEVSVSARNIRRLLSFQR----YLR 63
              | |   :   ||:| :     |: ::|     |:|:|:     |   :||:     ||
Db        263 RELTHLSEMSRSGNQVSEYISNTFLD-----KQNEVEIPSPTPRQR---AFQQPPPSVLR 314

Qy         64 SSR------FFRGTAVSNSLNI------LDDDYNGQAKCMLEKVGNWNFDIFLFDRLTNG 111
               |:      :    : |||      :  |         || :  |  :||       |
Db        315 QSQPMSQITGLKKLVHTGSLNTNVPRFGVKTDQEDLLAQELENLSKWGLNIFCVSEYAGG 374

Qy        112 NSLVSLTFHLFSLHGLIEYFHLDMMKLRRFLVMIQEDYHSQNPYHNAVHAADVTQAMHCY 171
              ||   : : :|    |:: ||: :  :  ::: ::: ||:   |||::|||| |: |
Db        375 RSLSCIMYTIFQERDLLKKFHIPVDTMMMYMLTLEDHYHADVAYHNSLHAADVLQSTHVL 434

Qy        172 LKEPKLANSVTPWDILLSLIAAATHDLDHPGVNQPFLIKTNHYLATLYKNTSVLENHHWR 231
              | | |    | :|| :| ||| ||:|||||:  ||| ||  || :| : |||||||
Db        435 LATPALDAVFTDLEILAALFAAAIHDVDHPGVSNQFLINTNSELALMYNDESVLENHHLA 494

Qy        232 SAVGLLRESG--LFSHLPLESRQQMETQIGALILATDISRQNEYLSLFRSHLD------R 283
                ||:|    :| :|    || :   :  ::||||:|:    |:  :: ::
Db        495 VGFKLLQEENCDIFQNLSKRQRQSLRKMVIDMVLATDMSKHMTLLADLKTMVETKKVTSS 554

Qy        284 GDLCLEDTRHRHLVLQMALKCADICNPCRTWELSKQWSEKVTEEFFHQGDIEKKYHLGVS 343
              | | |::   |  ||:  : |||: || :  || :||:::  ||| ||| |::  : :|
Db        555 GVLLLDNYSDRIQVLRNMVHCADLSNPTKPLELYRQWTDRIMAEFFQQGDRERERGMEIS 614

Qy        344 PLCDRHTESIANIQIGFMTYLVEPLFTEWA 373
              |:||:|| |:   |:||: |:| ||:  ||
Db        615 PMCDKHTASVEKSQVGFIDYIVHPLWETWA 644


RESULT 7
CN4A_MOUSE
ID   CN4A_MOUSE     STANDARD;      PRT;   844 AA.
AC   O89084; Q8R078; Q9JHQ4; Q9QX48; Q9QX49; Q9QXI8;
DT   28-FEB-2003 (Rel. 41, Created)
DT   28-FEB-2003 (Rel. 41, Last sequence update)
DT   10-OCT-2003 (Rel. 42, Last annotation update)
DE   cAMP-dependent 3',5'-cyclic phosphodiesterase 4A (EC 3.1.4.17).
GN   PDE4A.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.
RC   TISSUE=Embryonic stem cells;
RX   MEDLINE=20069070; PubMed=10602991;
RA   Olsen A.E., Bolger G.B.;
RT   "Physical mapping and promoter structure of the murine cAMP-specific
RT   phosphodiesterase pde4a gene.";
RL   Mamm. Genome 11:41-45(2000).
RN   [2]
RP   SEQUENCE FROM N.A. (ISOFORM 2), AND ENZYME REGULATION.
RC   TISSUE=Brain;
RX   MEDLINE=21167368; PubMed=11267656;
RA   Cherry J.A., Thompson B.E., Pho V.;
RT   "Diazepam and rolipram differentially inhibit cyclic AMP-specific
RT   phosphodiesterases PDE4A1 and PDE4B3 in the mouse.";
RL   Biochim. Biophys. Acta 1518:27-35(2001).
RN   [3]
RP   SEQUENCE FROM N.A. (ISOFORM 3).
RC   TISSUE=Salivary gland;
RX   MEDLINE=22388257; PubMed=12477932;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length
RT   human and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [4]
RP   SEQUENCE OF 248-355 FROM N.A. (ISOFORM 2).
RC   TISSUE=Brain;
RX   MEDLINE=98343959; PubMed=9677330;
RA   Sullivan M., Rena G., Begg F., Gordon L., Olsen A.S., Houslay M.D.;
RT   "Identification and characterization of the human homologue of the
RT   short PDE4A cAMP-specific phosphodiesterase 4A variant RD1 (PDE4A1) by
RT   analysis of the human HSPDE4A gene locus located at chromosome
RT   19p13.2.";
RL   Biochem. J. 333:693-703(1998).
CC   -!- CATALYTIC ACTIVITY: Adenosine 3',5'-cyclic phosphate + H(2)O =
CC       adenosine 5'-phosphate.
CC   -!- ENZYME REGULATION: Inhibited by rolipram and diazepam.
CC   -!- PATHWAY: Cyclic nucleotide metabolism.
CC   -!- ALTERNATIVE PRODUCTS:
CC       Event=Alternative splicing; Named isoforms=3;
CC         Comment=Additional isoforms seem to exist;
CC       Name=1;
CC         IsoId=O89084-1; Sequence=Displayed;
CC       Name=2;
CC         IsoId=O89084-2; Sequence=VSP_004563, VSP_004564;
CC       Name=3;
CC         IsoId=O89084-3; Sequence=VSP_004562;
CC   -!- SIMILARITY: Belongs to the cyclic nucleotide phosphodiesterase
CC       family.
CC   ---------------------------------------------------------------------
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CC   ---------------------------------------------------------------------
DR   EMBL; AF142646; AAF14519.1; -.
DR   EMBL; AF142643; AAF14519.1; JOINED.
DR   EMBL; AF142644; AAF14519.1; JOINED.
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DR   EMBL; AF142645; AAF14519.1; JOINED.
DR   EMBL; AF142646; AAF14520.1; -.
DR   EMBL; AF142644; AAF14520.1; JOINED.
DR   EMBL; AF142645; AAF14520.1; JOINED.
DR   EMBL; AJ297396; CAB96769.1; -.
DR   EMBL; BC027224; AAH27224.1; -.
DR   EMBL; AF208021; AAF19201.2; -.
DR   EMBL; U97586; AAC25681.1; -.
DR   MGD; MGI:99558; Pde4a.
DR   InterPro; IPR003607; Met_phsphohydro.
DR   InterPro; IPR002073; PDEase.
DR   Pfam; PF00233; PDEase; 1.
DR   PRINTS; PR00387; PDIESTERASE1.
DR   SMART; SM00471; HDc; 1.
DR   PROSITE; PS00126; PDEASE_I; 1.
KW   Hydrolase; cAMP; Alternative splicing; Multigene family.
FT   VARSPLIC      1    102       MEPPAAPSERSLSLSLPGPREGQATLKPPPQHLWRQPRTPI
FT                                RIQQRGYSDSAERSEPERSPHRPIERADAVDTGDRPGLRTT
FT                                RMSWPSSFHGTGTGGGSSRR -> MRSSAAPRARPRPPALA
FT                                LPLGPESLTHFSFSEEDTLRHPPGRCVS (in isoform
FT                                3).
FT                                /FTId=VSP_004562.
FT   VARSPLIC      1    234       Missing (in isoform 2).
FT                                /FTId=VSP_004563.
FT   VARSPLIC    235    256       WCLEQLETMQTYRSVSEMASHK -> MPLVDFFCETCSKPW
FT                                LVGWWDQ (in isoform 2).
FT                                /FTId=VSP_004564.
FT   CONFLICT    516    516       R -> K (IN REF. 2).
FT   CONFLICT    685    685       S -> G (IN REF. 3).
SQ   SEQUENCE   844 AA;  93558 MW;  632396C9F70E0F61 CRC64;

  Query Match             24.6%;  Score 551;  DB 1;  Length 844;
  Best Local Similarity   31.0%;  Pred. No. 2.2e-37;
  Matches  123;  Conservative   79;  Mismatches  149;  Indels   46;  Gaps    6;

Qy          8 RMLGDVRVRSRAGFESERRGSHPYIDFRIFHSQSEIEVS----------------VSAR 50
              | |   :   ||:| :      |: ::|      | |:|:                |:
Db        263 RELTHLSEMSRSGNQVSEYISNTFLD-----KQHEVEIPSPTPRQRPFQQPPPAAVQQAQ 317

Qy         51 NIRRLLSFQRYLRSSRFFRGTAVSNSLNI------LDDDYNGQAKCMLEKVGNWNFDIFL 104
               : ::   :: :             : ||||      :  |          || :  |  :||
Db        318 PMSQITGLKKLVH----------TGSLNINVPRFGVKTDQEDLLAQELENLSKWGLNIFC 367

Qy        105 FDRLTNGNSLVSLTFHLFSLHGLIEYFHLDMMKLRRFLVMIQEDYHSQNPYHNAVHAADV 164
                  | ||   : : :|     |:: ||: :  :  ::: ::: ||:   |||::|||||
Db        368 VSEYAGGRSLSCIMYTIFQERDLLKKFHIPVDTMMTYMLTLEDHYHADVAYHNSLHAADV 427

Qy        165 TQAMHCYLKEPKLANSVTPWDILLSLIAAATHDLDHPGVNQPFLIKTNHYLATLYKNTSV 224
              |: |   |  | |     |  :|| :| ||| ||:|||||:  ||| ||  || :| : ||
Db        428 LQSTHVLLATPALDAVFTDLEILAALFAAAIHDVDHPGVSNQFLINTNSELALMYNDESV 487

Qy        225 LENHHWRSAVGLLRESG--LFSHLPLESRQQMETQIGALILATDISRQNEYLSLFRSHLD 282
              |||||       ||:|    :| :|    || :   :  ::||||:|:    |:  :: ::
Db        488 LENHHLAVGFKLLQEENCDIFQNLSKRQRQSLRKMVIDMVLATDMSKHMTLLADLKTMVE 547

Qy        283 ------RGDLCLEDTRHRHLVLQMALKCADICNPCRTWELSKQWSEKVTEEFFHQGDIEK 336
                   | | |::   |  ||:  : |||: || :  || :||:::: |||  ||| |:
Db        548 TKKVTSSGVLLLDNYSDRIQVLRNMVHCADLSNPTKPLELYRQWTDRIMAEFFQQGDRER 607

Qy        337 KYHLGVSPLCDRHTESIANIQIGFMTYLVEPLFTEWA 373
              :  : :||:||:|| |:   |:||: |:| ||:  ||
Db        608 ERGMEISPMCDKHTASVEKSQVGFIDYIVHPLWETWA 644


RESULT 8
CN4B_RAT
ID   CN4B_RAT       STANDARD;      PRT;   721 AA.
AC   P14646;
DT   01-APR-1990 (Rel. 14, Created)
DT   15-JUL-1998 (Rel. 36, Last sequence update)
DT   28-FEB-2003 (Rel. 41, Last annotation update)
DE   cAMP-specific 3',5'-cyclic phosphodiesterase 4B (EC 3.1.4.17)
DE   (DPDE4).
GN   PDE4B.
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   SEQUENCE FROM N.A. (ISOFORM PDE4B3).
RA   Huston E., Simon L., Annette R., Catterall C., Ross A.H., Steele M.R.,
RA   Bolger G.B., Perry M., Owens R., Houslay M.D.;
RL   Submitted (MAR-1997) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   SEQUENCE OF 160-721 FROM N.A.
RC   TISSUE=Brain;
RX   MEDLINE=89264471; PubMed=2542941;
RA   Colicelli J., Birchmeier C., Michaeli T., O'Neill K., Riggs M.,
RA   Wigler M.;
RT   "Isolation and characterization of a mammalian gene encoding a high-
RT   affinity cAMP phosphodiesterase.";
RL   Proc. Natl. Acad. Sci. U.S.A. 86:3599-3603(1989).
RN   [3]
RP   SEQUENCE OF 289-638 FROM N.A.
RC   TISSUE=Testis;
RX   MEDLINE=89315790; PubMed=2546153;
RA   Swinnen J.V., Joseph D.R., Conti M.;
RT   "Molecular cloning of rat homologues of the Drosophila melanogaster
RT   dunce cAMP phosphodiesterase: evidence for a family of genes.";
RL   Proc. Natl. Acad. Sci. U.S.A. 86:5325-5329(1989).
RN   [4]
RP   SEQUENCE FROM N.A. (ISOFORM PDE4B2).
RX   MEDLINE=95047482; PubMed=7958996;
RA   Bolger G.B., Rodgers L., Riggs M.;
RT   "Differential CNS expression of alternative mRNA isoforms of the
RT   mammalian genes encoding cAMP-specific phosphodiesterases.";
RL   Gene 149:237-244(1994).
RN   [5]
RP   SEQUENCE FROM N.A. (ISOFORM PDE4B2).
RC   STRAIN=Wistar;
RX   MEDLINE=94103234; PubMed=8276818;
RA   Monaco L., Vicini E., Conti M.;
RT   "Structure of two rat genes coding for closely related rolipram-
RT   sensitive cAMP phosphodiesterases. Multiple mRNA variants originate
RT   from alternative splicing and multiple start sites.";
RL   J. Biol. Chem. 269:347-357(1994).
CC   -!- CATALYTIC ACTIVITY: Adenosine 3',5'-cyclic phosphate + H(2)O =
CC       adenosine 5'-phosphate.
CC   -!- ENZYME REGULATION: Inhibited by rolipram.
CC   -!- PATHWAY: Cyclic nucleotide metabolism.
CC   -!- ALTERNATIVE PRODUCTS:
CC       Event=Alternative splicing; Named isoforms=3;
CC         Comment=Additional isoforms seem to exist;
CC       Name=PDE4B3;
CC         IsoId=P14646-1; Sequence=Displayed;
CC       Name=PDE4B1;
CC         IsoId=P14646-3; Sequence=Not described;
CC       Name=PDE4B2;
CC         IsoId=P14646-2; Sequence=VSP_004573;
CC   -!- SIMILARITY: Belongs to the cyclic nucleotide phosphodiesterase
CC       family.
CC   ---------------------------------------------------------------------
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CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; U95748; AAB96560.1; -.
DR   EMBL; J04563; AAA66039.1; -.
DR   EMBL; M25350; AAA41846.1; -.
DR   EMBL; M28413; AAA41824.1; -.
DR   EMBL; L27058; AAA74478.1; -.
DR   EMBL; U01291; AAA18926.1; -.
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DR   EMBL; U01289; AAA18926.1; JOINED.
DR   EMBL; U01293; AAA18926.1; JOINED.
DR   EMBL; U01294; AAA18926.1; JOINED.
DR   EMBL; U01295; AAA18926.1; JOINED.
DR   EMBL; U01296; AAA18926.1; JOINED.
DR   EMBL; U01297; AAA18926.1; JOINED.
DR   EMBL; U01298; AAA18926.1; JOINED.
DR   EMBL; U01290; AAA18926.1; JOINED.
DR   PIR; A40949; A40949.
DR   PIR; I59143; I59143.
DR   InterPro; IPR003607; Met_phsphohydro.
DR   InterPro; IPR002073; PDEase.
DR   Pfam; PF00233; PDEase; 1.
DR   PRINTS; PR00387; PDIESTERASE1.
DR   SMART; SM00471; HDc; 1.
DR   PROSITE; PS00126; PDEASE_I; 1.
KW   Hydrolase; cAMP; Alternative splicing; Multigene family.
FT   VARSPLIC      1    196       MTAKNSSKELPASESEVCIKTFKEQMRLELELPKLPGNRPT
FT                                SPKISPRSSPRNSPCFFRKLLVNKSIRQRRRFTVAHTCFDV
FT                                ENGPSPGRSPLDPQASSSSGLVLHAAFPGHSQRRESFLYRS
FT                                DSDYDLSPKAMSRNSSLPSEQHGDDLIVTPFAQVLASLRIV
FT                                RNNFTLLTNLHGAPNKRSPAASQAPVTRVSLQ -> MKEQG
FT                                GTVSGAGSSRGGGDSAMASLQPLQPNYLSVCLFA (in
FT                                isoform PDE4B2).
FT                                /FTId=VSP_004573.
FT   CONFLICT    516    516       T -> S (IN REF. 5).
SQ   SEQUENCE   721 AA;  82100 MW;  C6FB885E6107BD4D CRC64;

  Query Match             24.5%;  Score 550;  DB 1;  Length 721;
  Best Local Similarity   31.8%;  Pred. No. 2.2e-37;
  Matches  122;  Conservative   84;  Mismatches  152;  Indels   26;  Gaps    6;

Qy          8 RMLGDVRVRSRAGFESERRGSHPYIDFRIFHSQSEIEVSVSARNIRR---------LLSF 58
              | |  :   ||:| :     |: ::|      |:::|:    :  |           :|
Db        241 RELTHLSEMSRSGNQVSEYISNTFLD-----KQNDVEIPSPTQKDREKKKKQQLMTQISG 295

Qy         59 QRYLRSSRFFRGTAVSN-SLNILDDDYNGQAKCMLEKVGNWNFDIFLFDRLTNGNSLVSL 117
               : |  |     |::|   :|  ::|:  :    || :  |  :||     ::   |  :
Db        296 VKKLMHSSSLNNTSISRFGVNTENEDHLAKE---LEDLNKWGLNIFNVAGYSHNRPLTCI 352

Qy        118 TFHLFSLHGLIEYFHLDMMKLRRFLVMIQEDYHSQNPYHNAVHAADVTQAMHCYLKEPKL 177
              : :|    |:: | :       ::: ::: |||   |||::|||| |: |  |  | |
Db        353 MYAIFQERDLLKTFKISSDTFVTYMMTLEDHYHSDVAYHNSLHAADVAQSTHVLLSTPAL 412

Qy        178 ANSVTPWDILLSLIAAATHDLDHPGVNQPFLIKTNHYLATLYKNTSVLENHHWRSAVGLL 237
              |  :|| :: ||| ||:|||||:  ||| ||  || :| : |||||||      ||
Db        413 DAVFTDLEILAAIFAAAIHDVDHPGVSNQFLINTNSELALMYNDESVLENHHLAVGFKLL 472

Qy        238 RES--GLFSHLPLESRQQMETQIGALILATDISRQNEYLSLFRSHLD------RGDLCLE 289
              :|    :| :|  : || :   :  ::||||:|:    |:  :: ::       | | |:
Db        473 QEEHCDIFQNLTKKQRQTLRKMVIDMVLATDMSKHMSLLADLKTMVETKKVTSSGVLLLD 532

Qy        290 DTRHRHLVLQMALKCADICNPCRTWELSKQWSEKVTEEFFHQGDIEKKYHLGVSPLCDRH 349
              :   |  ||:  : |||: || :: || :|:|:::: |||| ||| |::  : :||:||:|
Db        533 NYTDRIQVLRNMVHCADLSNPTKSLELYRQWTDRIMEEFFQQGDKERERGMEISPMCDKH 592

Qy        350 TESIANIQIGFMTYLVEPLFTEWA 373
              | |:   |:||: |:| ||:  ||
Db        593 TASVEKSQVGFIDYIVHPLWETWA 616


RESULT 9
CN4B_HUMAN
ID   CN4B_HUMAN     STANDARD;      PRT;   736 AA.
AC   Q07343; O15443;
DT   01-FEB-1995 (Rel. 31, Created)
DT   01-FEB-1995 (Rel. 31, Last sequence update)
DT   15-MAR-2004 (Rel. 43, Last annotation update)
DE   cAMP-specific 3',5'-cyclic phosphodiesterase 4B (EC 3.1.4.17)
DE   (DPDE4) (PDE32).
GN   PDE4B.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A. (ISOFORMS PDE4B1 AND PDE4B2).
RC   TISSUE=Brain;
RX   MEDLINE=94019330; PubMed=8413254;
RA   Bolger G., Michaeli T., Martins T., St John T., Steiner B.,
RA   Rodgers L., Riggs M., Wigler M., Ferguson K.;
RT   "A family of human phosphodiesterases homologous to the dunce
RT   learning and memory gene product of Drosophila melanogaster are
RT   potential targets for antidepressant drugs.";
RL   Mol. Cell. Biol. 13:6558-6571(1993).
RN   [2]
RP   SEQUENCE FROM N.A. (ISOFORM PDE4B3).
RX   MEDLINE=98041898; PubMed=9371714;
RA   Huston E., Lumb S., Russell A., Catterall C., Ross A.H., Steele M.R.,
RA   Bolger G.B., Perry M.J., Owens R.J., Houslay M.D.;
RT   "Molecular cloning and transient expression in COS7 cells of a novel
RT   human PDE4B cAMP-specific phosphodiesterase, HSPDE4B3.";
RL   Biochem. J. 328:549-558(1997).
RN   [3]
RP   SEQUENCE FROM N.A. (ISOFORM PDE4B2).
RC   TISSUE=Brain;
RX   MEDLINE=93203241; PubMed=8384210;
RA   McLaughlin M.M., Cieslinski L.B., Burman M., Torphy T.J.,
RA   Livi G.P.;
RT   "A low-Km, rolipram-sensitive, cAMP-specific phosphodiesterase from
RT   human brain. Cloning and expression of cDNA, biochemical
RT   characterization of recombinant protein, and tissue distribution of
RT   mRNA.";
RL   J. Biol. Chem. 268:6470-6476(1993).
CC   -!- FUNCTION: May be involved in mediating central nervous system
CC       effects of therapeutic agents ranging from antidepressants to
CC       antiasthmatic and anti-inflammatory agents.
CC   -!- CATALYTIC ACTIVITY: Adenosine 3',5'-cyclic phosphate + H(2)O =
CC       adenosine 5'-phosphate.
CC   -!- ENZYME REGULATION: Inhibited by rolipram.
CC   -!- PATHWAY: Cyclic nucleotide metabolism.
CC   -!- ALTERNATIVE PRODUCTS:
CC       Event=Alternative splicing; Named isoforms=3;
CC         Comment=Additional isoforms seem to exist;
CC       Name=PDE4B1;
CC         IsoId=Q07343-1; Sequence=Displayed;
CC       Name=PDE4B2;
CC         IsoId=Q07343-2; Sequence=VSP_004572;
CC       Name=PDE4B3;
CC         IsoId=Q07343-3; Sequence=VSP_004571;
CC   -!- TISSUE SPECIFICITY: Expressed in brain, heart, lung and skeletal
CC       muscle.
CC   -!- SIMILARITY: Belongs to the cyclic nucleotide phosphodiesterase
CC       family.
CC   ---------------------------------------------------------------------
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CC   ---------------------------------------------------------------------
DR   EMBL; L20966; AAA03589.1; -.
DR   EMBL; L20971; AAA03593.1; -.
DR   EMBL; M97515; AAA36426.1; -.
DR   EMBL; U85048; AAB96381.1; -.
DR   PIR; I61354; I61354.
DR   PDB; 1F0J; 26-JUL-00.
DR   PDB; 1JP1; 16-JAN-02.
DR   PDB; 1JP2; 16-JAN-02.
DR   Genew; HGNC:8781; PDE4B.
DR   MIM; 600127; -.
DR   GO; GO:0005626; C:insoluble fraction; TAS.
DR   GO; GO:0005625; C:soluble fraction; TAS.
DR   GO; GO:0004115; F:cAMP-specific phosphodiesterase activity; TAS.
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DR   InterPro; IPR003607; Met_phsphohydro.
DR   InterPro; IPR002073; PDEase.
DR   Pfam; PF00233; PDEase; 1.
DR   PRINTS; PR00387; PDIESTERASE1.
DR   SMART; SM00471; HDc; 1.
DR   PROSITE; PS00126; PDEASE_I; 1.
KW   Hydrolase; cAMP; Alternative splicing; Multigene family; 3D-structure.
FT   VARSPLIC      1     93       MKKSRSVMTVMADDNVKDYFECSLSKSYSSSSNTLGIDLWR
FT                                GRRCCSGNLQLPPLSQRQSERARTPEGDGISRPTTLPLTTL
FT                                PSIAITTVSQE -> MTAKDSSKELTASEPEVCIKTFKEQM
FT                                HLELELPRLPGNRPTSPKISPRSSPRNSPCFFRKLLVNKSI
FT                                RQRRRFTVAHT (in isoform PDE4B3).
FT                                /FTId=VSP_004571.
FT   VARSPLIC      1    211       MKKSRSVMTVMADDNVKDYFECSLSKSYSSSSNTLGIDLWR
FT                                GRRCCSGNLQLPPLSQRQSERARTPEGDGISRPTTLPLTTL
FT                                PSIAITTVSQECFDVENGPSPGRSPLDPQASSSAGLVLHAT
FT                                FPGHSQRRESFLYRSDSDYDLSPKAMSRNSSLPSEQHGDDL
FT                                IVTPFAQVLASLRSVRNNFTILTNLHGTSNKRSPAASQPPV
FT                                SRVNPQ -> MKKEHGGTFSSTGISGGSGDSAMDSLQPLQP
FT                                NYMPVCLFA (in isoform PDE4B2).
FT                                /FTId=VSP_004572.
SQ   SEQUENCE   736 AA;  83343 MW;  208FCE9CD40EF5EB CRC64;

  Query Match             24.5%;  Score 550;  DB 1;  Length 736;
  Best Local Similarity   31.8%;  Pred. No. 2.3e-37;
  Matches  122;  Conservative   84;  Mismatches  152;  Indels   26;  Gaps    6;

Qy          8 RMLGDVRVRSRAGFESERRGSHPYIDFRIFHSQSEIEVSVSARNIRR---------LLSF 58
              |  |   :   ||:| :     |: ::|      |:::|:   :  |           :|
Db        256 RELTHLSEMSRSGNQVSEYISNTFLD-----KQNDVEIPSPTQKDREKKKKQQLMTQISG 310

Qy         59 QRYLRSSRFFRGTAVSN-SLNILDDDYNGQAKCMLEKVGNWNFDIFLFDRLTNGNSLVSL 117
               :  |     |::|   :|  ::|:  :    || :  |  :||     ::   |  :
Db        311 VKKLMHSSSLNNTSISRFGVNTENEDHLAKE---LEDLNKWGLNIFNVAGYSHNRPLTCI 367

Qy        118 TFHLFSLHGLIEYFHLDMMKLRRFLVMIQEDYHSQNPYHNAVHAADVTQAMHCYLKEPKL 177
              : :|    |:: | :       ::: ::: |||   |||::|||||  |: |  |  | |
Db        368 MYAIFQERDLLKTFRISSDTFITYMMTLEDHYHSDVAYHNSLHAADVAQSTHVLLSTPAL 427

Qy        178 ANSVTPWDILLSLIAAATHDLDHPGVNQPFLIKTNHYLATLYKNTSVLENHHWRSAVGLL 237
                |  :|| :: ||| ||:|||||:  ||| ||  || :| : |||||||      ||
Db        428 DAVFTDLEILAAIFAAAIHDVDHPGVSNQFLINTNSELALMYNDESVLENHHLAVGFKLL 487

Qy        238 RES--GLFSHLPLESRQQMETQIGALILATDISRQNEYLSLFRSHLD------RGDLCLE 289
              :|    :| :|  : || :   :  ::||||:|:    |:  :: ::       | | |:
Db        488 QEEHCDIFMNLTKKQRQTLRKMVIDMVLATDMSKHMSLLADLKTMVETKKVTSSGVLLLD 547

Qy        290 DTRHRHLVLQMALKCADICNPCRTWELSKQWSEKVTEEFFHQGDIEKKYHLGVSPLCDRH 349
              :  |  ||:  : |||: || :: || :||:::: |||| ||| |::  : :||:||:|
Db        548 NYTDRIQVLRNMVHCADLSNPTKSLELYRQWTDRIMEEFFQQGDKERERGMEISPMCDKH 607

Qy        350 TESIANIQIGFMTYLVEPLFTEWA 373
              | |:   |:||: |:| ||:  ||
Db        608 TASVEKSQVGFIDYIVHPLWETWA 631


RESULT 10
CN4C_HUMAN
ID   CN4C_HUMAN     STANDARD;      PRT;   712 AA.
AC   Q08493; Q9UN44; Q9UN45; Q9UN46; Q9UPJ6;
DT   01-OCT-1996 (Rel. 34, Created)
DT   28-FEB-2003 (Rel. 41, Last sequence update)
DT   10-OCT-2003 (Rel. 42, Last annotation update)
DE   cAMP-specific 3',5'-cyclic phosphodiesterase 4C (EC 3.1.4.17)
DE   (DPDE1) (PDE21).
GN   PDE4C.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A. (ISOFORM PDE4C1).
RC   TISSUE=Substantia nigra;
RX   MEDLINE=95145731; PubMed=7843419;
RA   Engels P., Sullivan M., Mueller T., Luebbert H.;
RT   "Molecular cloning and functional expression in yeast of a human
RT   cAMP-specific phosphodiesterase subtype (PDE IV-C).";
RL   FEBS Lett. 358:305-310(1995).
RN   [2]
RP   SEQUENCE FROM N.A. (ISOFORMS PDE4C1; PDE4C2 AND PDE4C3).
RX   MEDLINE=20039485; PubMed=10574328;
RA   Sullivan M., Olsen A.S., Houslay M.D.;
RT   "Genomic organisation of the human cyclic AMP-specific
RT   phosphodiesterase PDE4C gene and its chromosomal localisation to
RT   19p13.1, between RAB3A and JUND.";
RL   Cell. Signal. 11:735-742(1999).
RN   [3]
RP   SEQUENCE FROM N.A.
RA   Lamerdin J.E., McCready P.M., Skowronski E., Viswanathan V.,
RA   Burkhart-Schultz K., Gordon L., Dias J., Ramirez M., Stilwagen S.,
RA   Phan H., Velasco N., Do L., Regala W., Terry A., Garnes J.,
RA   Danganan L., Poundstone P., Christensen M., Georgescu A., Avila J.,
RA   Liu S., Attix C., Andreise T., Trankheim M., Amico-Keller G.,
RA   Coefield J., Duarte S., Lucas S., Bruce R., Thomas P., Quan G.,
RA   Kronmiller B., Arellano A., Saunders C., Ow D., Nolan M., Trong S.,
RA   Kobayashi A., Olsen A.S., Carrano A.V.;
RT   "Sequence analysis of an ~600 kb region in 19p13.1 between JAK3 and
RT   PDE4C.";
RL   Submitted (OCT-1998) to the EMBL/GenBank/DDBJ databases.
RN   [4]
RP   SEQUENCE OF 462-712 FROM N.A.
RX   MEDLINE=94019330; PubMed=8413254;
RA   Bolger G., Michaeli T., Martins T., St John T., Steiner B.,
RA   Rodgers L., Riggs M., Wigler M., Ferguson K.;
RT   "A family of human phosphodiesterases homologous to the dunce
RT   learning and memory gene product of Drosophila melanogaster are
RT   potential targets for antidepressant drugs.";
RL   Mol. Cell. Biol. 13:6558-6571(1993).
CC   -!- CATALYTIC ACTIVITY: Adenosine 3',5'-cyclic phosphate + H(2)O =
CC       adenosine 5'-phosphate.
CC   -!- ENZYME REGULATION: Inhibited by rolipram.
CC   -!- PATHWAY: Cyclic nucleotide metabolism.
CC   -!- ALTERNATIVE PRODUCTS:
CC       Event=Alternative splicing; Named isoforms=7;
CC       Name=PDE4C1;
CC         IsoId=Q08493-1; Sequence=Displayed;
CC       Name=PDE4C2;
CC         IsoId=Q08493-2; Sequence=VSP_004575;
CC       Name=PDE4C3;
CC         IsoId=Q08493-3; Sequence=VSP_004574;
CC       Name=PDE4C4;
CC         IsoId=Q08493-4; Sequence=Not described;
CC       Name=PDE4C5;
CC         IsoId=Q08493-5; Sequence=Not described;
CC       Name=PDE4C6;
CC         IsoId=Q08493-6; Sequence=Not described;
CC       Name=PDE4C7;
CC         IsoId=Q08493-7; Sequence=Not described;
CC   -!- TISSUE SPECIFICITY: EXPRESSED IN VARIOUS TISSUES BUT NOT IN CELLS
CC       OF THE IMMUNE SYSTEM.
CC   -!- SIMILARITY: Belongs to the cyclic nucleotide phosphodiesterase
CC       family.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; Z46632; CAA86601.1; -.
DR   EMBL; AF157816; AAD47053.1; -.
DR   EMBL; AF157811; AAD47053.1; JOINED.
DR   EMBL; AF157814; AAD47053.1; JOINED.
DR   EMBL; AF157815; AAD47053.1; JOINED.
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DR   EMBL; AF157816; AAD47054.1; -.
DR   EMBL; AF157812; AAD47054.1; JOINED.
DR   EMBL; AF157814; AAD47054.1; JOINED.
DR   EMBL; AF157815; AAD47054.1; JOINED.
DR   EMBL; AF157816; AAD47055.1; -.
DR   EMBL; AF157814; AAD47055.1; JOINED.
DR   EMBL; AF157815; AAD47055.1; JOINED.
DR   EMBL; AC005759; AAC83047.1; -.
DR   EMBL; L20968; AAA03591.1; -.
DR   PIR; S71626; S71626.
DR   PDB; 1LXU; 26-JUN-02.
DR   Genew; HGNC:8782; PDE4C.
DR   MIM; 600128; -.
DR   GO; GO:0004115; F:cAMP-specific phosphodiesterase activity; TAS.
DR   InterPro; IPR003607; Met_phsphohydro.
DR   InterPro; IPR002073; PDEase.
DR   Pfam; PF00233; PDEase; 1.
DR   PRINTS; PR00387; PDIESTERASE1.
DR   SMART; SM00471; HDc; 1.
DR   PROSITE; PS00126; PDEASE_I; 1.
KW   Hydrolase; cAMP; Multigene family; Alternative splicing; 3D-structure.
FT   VARSPLIC      1     81       MENLGVGEGAEACSRLSRSRGRHSMTRAPKHLWRQPRRPIR
FT                                IQQRFYSDPDKSAGCRERDLSPRPELRKSRLSWPVSSCRR
FT                                -> MQGPPAPAPVPGPGSPRGSPRGSPGLFRKLLVNQSIRL
FT                                QRRFTVAHPLC (in isoform PDE4C3).
FT                                /FTId=VSP_004574.
FT   VARSPLIC      1    106       Missing (in isoform PDE4C2).
FT                                /FTId=VSP_004575.
FT   CONFLICT    204    204       K -> N (IN REF. 2).
FT   CONFLICT    211    211       D -> Y (IN REF. 2).
FT   CONFLICT    339    340       EL -> DV (IN REF. 1).
FT   CONFLICT    444    446       NSE -> K (IN REF. 3).
FT   CONFLICT    446    447       EL -> DV (IN REF. 1).
SQ   SEQUENCE   712 AA;  79901 MW;  1932116C9CE0322C CRC64;

  Query Match           24.3%;  Score 545;  DB 1;  Length 712;
  Best Local Similarity  33.8%;  Pred. No. 5.6e-37;
  Matches  125;  Conservative   68;  Mismatches  153;  Indels   24;  Gaps    7;

Qy         22 ESERRGSH--PYIDFRIFHSQSEIEV-SVSARNIRRLLSFQRYLRSSRFFRGTAVSNSLN 78
              }: } |:    ||       |:|:|:  |:|    : :|     | |    |   | ||:
Db        250 ETSRSGNQVSEYISRTFLDQQTEVELPKVTAEEAPQPMS-----RISG-LHGLCHSASLS 303

Qy         79 I-------LDDDYNGQAKCMLEKVGNWNFDIFLFDRLTNGNSLVSLTFHLFSLHGLIEYF 131
                  :  |    |    ||     |  |:|    |:    | :: | :|    |:: |
Db        304 SATVPRFGVQTDQEEQLAKELEDTNKWGLDVFKVAELSGNRPLTAIIFSIFQERDLLKTF 363

Qy        132 HLDMMKLRRFLVMIQEDYHSQNPYHNAVHAADVTQAMHCYLKEPKLANSVTPWDILLSLI 191
               :    | :|:|::  ||:   |||::|||||  |: |  |  | |     |  :|| :|
Db        364 QIPADTLATYLLMLEGHYHANVAYHNSLHAADVAQSTHVLLATPALEAVFTDLEILAALF 423

Qy        192 AAATHDLDHPGVNQPFLIKTNHYLATLYKNTSVLENHHWRSAVGLLRESG--LFSHLPLE 249
              |:| ||:|||||:  ||| ||  || :| : |||||||      ||:     :| :|  :
Db        424 ASAIHDVDHPGVSNQFLINTNSELALMYNDASVLENHHLAVGFKLLQAENCDIFQNLSAK 483

Qy        250 SRQQMETQIGALILATDISRQNEYLSLFRSHLDR------GDLCLEDTRHRHLVLQMALK 303
               |  :   :  ::||||:|:    |:  :: ::       | | |::   |  |||  :
Db        484 QRLSLRRMVIDMVLATDMSKHMNLLADLKTMVETKKVTSLGVLLLDNYSDRIQVLQNLVH 543

Qy        304 CADICNPCRTWELSKQWSEKVTEEFFHQGDIEKKYHLGVSPLCDRHTESIANIQIGFMTY 363
              |||: || :   | :||:::  ||| ||| |::  | :||:||:|| |:   |:||: |
Db        544 CADLSNPTKPLPLYRQWTDRIMAEFFQQGDRERESGLDISPMCDKHTASVEKSQVGFIDY 603

Qy        364 LVEPLFTEWA 373
               :  ||:  ||
Db        604 IAHPLWETWA 613


RESULT 11
CN4D_HUMAN
ID   CN4D_HUMAN     STANDARD;      PRT;   809 AA.
AC   Q08499; O43433; Q13549; Q13550; Q13551;
DT   01-OCT-1996 (Rel. 34, Created)
DT   16-OCT-2001 (Rel. 40, Last sequence update)
DT   10-OCT-2003 (Rel. 42, Last annotation update)
DE   cAMP-specific 3',5'-cyclic phosphodiesterase 4D (EC 3.1.4.17)
DE   (DPDE3) (PDE43).
GN   PDE4D.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
RX   MEDLINE=94019330; PubMed=8413254;
RA   Bolger G., Michaeli T., Martins T., John T., Steiner B.,
RA   Rodgers L., Riggs M., Wigler M., Ferguson K.;
RT   "A family of human phosphodiesterases homologous to the dunce
RT   learning and memory gene product of Drosophila melanogaster are
RT   potential targets for antidepressant drugs.";
RL   Mol. Cell. Biol. 13:6558-6571(1993).
RN   [2]
RP   SEQUENCE FROM N.A. (ISOFORMS 1; 2; 3; 4; 5 AND 6), AND REVISIONS TO
RP   ISOFORM 1.
RX   MEDLINE=98041897; PubMed=9371713;
RA   Bolger G.B., Erdogan S., Jones R.E., Loughney K., Scotland G.,
RA   Hoffmann R., Wilkinson I., Farrell C., Houslay M.D.;
RT   "Characterization of five different proteins produced by
RT   alternatively spliced mRNAs from the human cAMP-specific
RT   phosphodiesterase PDE4D gene.";
RL   Biochem. J. 328:539-548(1997).
RN   [3]
RP   SEQUENCE FROM N.A. (ISOFORM 3).
RC   TISSUE=Heart;
RX   MEDLINE=94171048; PubMed=8125310;
RA   Baecker P.A., Obernolte R., Bach C., Yee C., Shelton E.R.;
RT   "Isolation of a cDNA encoding a human rolipram-sensitive cyclic AMP
RT   phosphodiesterase (PDE IVD).";
RL   Gene 138:253-256(1994).
RN   [4]
RP   SEQUENCE FROM N.A. (ISOFORMS 1; 4 AND 5).
RX   MEDLINE=96390839; PubMed=8797812;
RA   Nemoz G., Zhang R.B., Sette C., Conti M.;
RT   "Identification of cyclic AMP-phosphodiesterase variants from the
RT   PDE4D gene expressed in human peripheral mononuclear cells.";
RL   FEBS Lett. 384:97-102(1996).
CC   -!- CATALYTIC ACTIVITY: Adenosine 3',5'-cyclic phosphate + H(2)O =
CC       adenosine 5'-phosphate.
CC   -!- ENZYME REGULATION: Inhibited by rolipram.
CC   -!- PATHWAY: Cyclic nucleotide metabolism.
CC   -!- ALTERNATIVE PRODUCTS:
CC       Event=Alternative splicing; Named isoforms=6;
CC       Name=1; Synonyms=hPDE4D4;
CC         IsoId=Q08499-1; Sequence=Displayed;
CC       Name=2; Synonyms=hPDE4D3;
CC         IsoId=Q08499-2; Sequence=VSP_004577;
CC       Name=3;
CC         IsoId=Q08499-3; Sequence=VSP_004578;
CC       Name=4; Synonyms=hPDE4D1;
CC         IsoId=Q08499-4; Sequence=VSP_004579;
CC       Name=5; Synonyms=hPDE4D2;
CC         IsoId=Q08499-5; Sequence=VSP_004580;
CC       Name=6; Synonyms=hPDE4D5;
CC         IsoId=Q08499-6; Sequence=VSP_004576;
CC   -!- TISSUE SPECIFICITY: WIDESPREAD; MOST ABUNDANT IN SKELETAL MUSCLE.
CC   -!- SIMILARITY: Belongs to the cyclic nucleotide phosphodiesterase
CC       family.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
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DR   EMBL; L20970; AAA03592.1; -.
DR   EMBL; L20969; AAC00042.1; -.
DR   EMBL; U02882; AAC13745.1; -.
DR   EMBL; U50157; AAA97890.1; -.
DR   EMBL; U50158; AAA97891.1; -.
DR   EMBL; U50159; AAA97892.1; -.
DR   EMBL; AF012074; AAC00070.1; -.
DR   EMBL; AF012073; AAC00069.1; -.
DR   PDB; 1MKD; 01-MAR-03.
DR   Genew; HGNC:8783; PDE4D.
DR   MIM; 600129; -.
DR   GO; GO:0005626; C:insoluble fraction; TAS.
DR   GO; GO:0005625; C:soluble fraction; TAS.
DR   GO; GO:0004115; F:cAMP-specific phosphodiesterase activity; TAS.
DR   InterPro; IPR003607; Met_phsphohydro.
DR   InterPro; IPR002073; PDEase.
DR   Pfam; PF00233; PDEase; 1.
DR   PRINTS; PR00387; PDIESTERASE1.
DR   SMART; SM00471; HDc; 1.
DR   PROSITE; PS00126; PDEASE_I; 1.
KW   Hydrolase; cAMP; Alternative splicing; Multigene family; 3D-structure.
FT   VARSPLIC      1    152       MEAEGSSAPARAGSGEGSDSAGGATLKAPKHLWRHEQHHQY
FT                                PLRQPQFRLLHPHHHLPPPPPPSPQPQPQCPLQPPPPPPLP
FT                                PPPPPPGAARGRYASSGATGRVRHRGYSDTERYLYCRAMDR
FT                                TSYAVETGHRPGLKKSRMSWPSSFQGLRR -> MAQQTSPD
FT                                (in isoform 6).
FT                                /FTId=VSP_004576.
FT   VARSPLIC      1    152       MEAEGSSAPARAGSGEGSDSAGGATLKAPKHLWRHEQHHQY
FT                                PLRQPQFRLLHPHHHLPPPPPPSPQPQPQCPLQPPPPPPLP
FT                                PPPPPPGAARGRYASSGATGRVRHRGYSDTERYLYCRAMDR
FT                                TSYAVETGHRPGLKKSRMSWPSSFQGLRR -> MMHVNNFF
FT                                RRHSWIC (in isoform 2).
FT                                /FTId=VSP_004577.
FT   VARSPLIC      1    205       Missing (in isoform 3).
FT                                /FTId=VSP_004578.
FT   VARSPLIC      1    269       MEAEGSSAPARAGSGEGSDSAGGATLKAPKHLWRHEQHHQY
FT                                PLRQPQFRLLHPHHHLPPPPPPSPQPQPQCPLQPPPPPPLP
FT                                PPPPPPGAARGRYASSGATGRVRHRGYSDTERYLYCRAMDR
FT                                TSYAVETGHRPGLKKSRMSWPSSFQGLRRFDVDNGTSAGRS
FT                                PLDPMTSPGSGLILQANFVHSQRRESFLYRSDSDYDLSPKS
FT                                MSRNSSIASDIHGDDLIVTPFAQVLASLRTVRNNFAALTNL
FT                                QDRAPSKRSPMCNQPSINKATIT -> MKEQPSCAGTGHPM
FT                                AGYGRMAPFELASGPVKRLRTESPFPCLFA (in
FT                                isoform 4).
FT                                /FTId=VSP_004579.
FT   VARSPLIC      1    302       Missing (in isoform 5).
FT                                /FTId=VSP_004580.
FT   CONFLICT    644    644       R -> P (IN REF. 3).
FT   CONFLICT    769    769       C -> R (IN REF. 4).
SQ   SEQUENCE   809 AA;  91114 MW;  7A4773DD3A044F57 CRC64;

  Query Match             24.2%;  Score 542;  DB 1;  Length 809;
  Best Local Similarity   31.6%;  Pred. No. 1.2e-36;
  Matches  122;  Conservative   82;  Mismatches  150;  Indels   32;  Gaps    7;

Qy          8 RMLGDVRVRSRAGFESERRGSHPYIDFRIFHSQSEIEV--------SVSARNIRRLLSFQ 59
              | |   :   ||:| :     |: ::|      | |:|:            | : ::   :
Db        314 RELTHLSEMSRSGNQVSEFISNTFLD-----KQHEVEIPSPTQKEKEKKKRPMSQISGVK 368

Qy         60 RYLRSSRFFRGTAVSNS----LNILDDDYNGQAKCMLEKVGNWNFDIFLFDRLTNGNSLV 115
              : : ||      :::||      :  :  :  ||  || |  |   :|    |:    |
Db        369 KLMHSS------SLTNSSIPRFGVKTEQEDVLAK-ELEDVNKWGLHVFRIAELSGNRPLT 421

Qy        116 SLTFHLFSLHGLIEYFHLDMMKLRRFLVMIQEDYHSQNPYHNAVHAADVTQAMHCYLKEP 175
              :   :|    |:: | : :  |  :|: ::: ||:   ||| :|||| |: |  |  |
Db        422 VIMHTIFQERDLLKTFKIPVDTLITYLMTLEDHYHADVAYHNNIHAADVVQSTHVLLSTP 481

Qy        176 KLANSVTPWDILLSLIAAATHDLDHPGVNQPFLIKTNHYLATLYKNTSVLENHHWRSAVG 235
              |    |  :|| :: |:| ||:|||||:  ||| ||  || :| ::|||||||
Db        482 ALEAVFTDLEILAAIFASAIHDVDHPGVSNQFLINTNSELALMYNDSSVLENHHLAVGFK 541

Qy        236 LLRESG--LFSHLPLESRQQMETQIGALILATDISRQNEYLSLFRSHLD------RGDLC 287
              ||:|    :| :|  : || :   :  ::||||:|:    |:  :: ::       | |
Db        542 LLQEENCDIFQNLTKKQRQSLRKMVIDIVLATDMSKHMNLLADLKTMVETKKVTSSGVLL 601

Qy        288 LEDTRHRHLVLQMALKCADICNPCRTWELSKQWSEKVTEEFFHQGDIEKKYHLGVSPLCD 347
              |::   |  |||  : |||: || :  :| :||:::: |||| ||| |::  : :||:||
Db        602 LDNYSDRIQVLQNMVHCADLSNPTKPLQLYRQWTDRIMEEFFRQGDRERERGMEISPMCD 661

Qy        348 RHTESIANIQIGFMTYLVEPLFTEWA 373
              :|  |:   |:||: |:| ||:  ||
Db        662 KHNASVEKSQVGFIDYIVHPLWETWA 687


RESULT 12
CN4A_HUMAN
ID   CN4A_HUMAN     STANDARD;      PRT;   886 AA.
AC   P27815; O75522; O76092; Q16255; Q16691; Q8WUQ3;
DT   01-AUG-1992 (Rel. 23, Created)
DT   01-OCT-1996 (Rel. 34, Last sequence update)
DT   10-OCT-2003 (Rel. 42, Last annotation update)
DE   cAMP-specific 3',5'-cyclic phosphodiesterase 4A (EC 3.1.4.17)
DE   (DPDE2) (PDE46).
GN   PDE4A.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A. (ISOFORM 1).
RX   MEDLINE=94019330; PubMed=8413254;
RA   Bolger G., Michaeli T., Martins T., St John T., Steiner B.,
RA   Rodgers L., Riggs M., Wigler M., Ferguson K.;
RT   "A family of human phosphodiesterases homologous to the dunce
RT   learning and memory gene product of Drosophila melanogaster are
RT   potential targets for antidepressant drugs.";
RL   Mol. Cell. Biol. 13:6558-6571(1993).
RN   [2]
RP   SEQUENCE FROM N.A. (ISOFORMS 1; 2; 3; 4 AND 5).
RC   TISSUE=Brain;
RX   MEDLINE=98343959; PubMed=9677330;
RA   Sullivan M., Rena G., Begg F., Gordon L., Olsen A.S., Houslay M.D.;
RT   "Identification and characterization of the human homologue of the
RT   short PDE4A cAMP-specific phosphodiesterase RD1 (PDE4A1) by analysis
RT   of the human HSPDE4A gene locus located at chromosome 19p13.2.";
RL   Biochem. J. 333:693-703(1998).
RN   [3]
RP   SEQUENCE OF 112-886 FROM N.A.
RC   TISSUE=Monocytes;
RX   MEDLINE=90258854; PubMed=2160582;
RA   Livi G.P., Kmetz P., McHale M.M., Cieslinski L.B., Sathe G.M.,
RA   Taylor D.P., Davis R.L., Torphy T.J., Balcarek J.M.;
RT   "Cloning and expression of cDNA for a human low-Km, rolipram-sensitive
RT   cyclic AMP phosphodiesterase.";
RL   Mol. Cell. Biol. 10:2678-2686(1990).
RN   [4]
RP   REVISIONS TO REF.3.
RA   McLaughlin M.M.;
RL   Submitted (JAN-1991) to the EMBL/GenBank/DDBJ databases.
RN   [5]
RP   SEQUENCE FROM N.A. (ISOFORMS 3 AND 5).
RX   MEDLINE=95290008; PubMed=7772058;
RA   Horton Y.M., Sullivan M., Houslay M.D.;
RT   "Molecular cloning of a novel splice variant of human type IVA
RT   (PDE-IVA) cyclic AMP phosphodiesterase and localization of the gene
RT   to the p13.2-q12 region of human chromosome 19.";
RL   Biochem. J. 308:683-691(1995).
RN   [6]
RP   SEQUENCE FROM N.A. (ISOFORM 3).
RX   MEDLINE=95194817; PubMed=7888306;
RA   Sullivan M., Egerton M., Shakur Y., Marquardsen A., Houslay M.D.;
RT   "Molecular cloning and expression, in both COS-1 cells and S.
RT   cerevisiae, of a human cytosolic type-IVA, cyclic AMP specific
RT   phosphodiesterase (hPDE-IVA-h6.1).";
RL   Cell. Signal. 6:793-812(1994).
RN   [7]
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RP   SEQUENCE FROM N.A. (ISOFORM 4).
RC   TISSUE=Brain;
RX   MEDLINE=22388257; PubMed=12477932;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length
RT   human and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC   -!- CATALYTIC ACTIVITY: Adenosine 3',5'-cyclic phosphate + H(2)O =
CC       adenosine 5'-phosphate.
CC   -!- ENZYME REGULATION: Inhibited by rolipram.
CC   -!- PATHWAY: Cyclic nucleotide metabolism.
CC   -!- SUBCELLULAR LOCATION: Isoform 4 has propensity for association
CC       with membranes.
CC   -!- ALTERNATIVE PRODUCTS:
CC       Event=Alternative splicing; Named isoforms=5;
CC         Comment=Additional isoforms seem to exist;
CC       Name=1; Synonyms=PDE46;
CC         IsoId=P27815-1; Sequence=Displayed;
CC       Name=2; Synonyms=TM3;
CC         IsoId=P27815-2; Sequence=VSP_004556;
CC       Name=3; Synonyms=PDE4A7, PDE4A6;
CC         IsoId=P27815-3; Sequence=VSP_004557;
CC       Name=4; Synonyms=PDE4A1, RD1;
CC         IsoId=P27815-4; Sequence=VSP_004558;
CC       Name=5; Synonyms=PDE4A8, 2EL;
CC         IsoId=P27815-5; Sequence=VSP_004559, VSP_004560, VSP_004561;
CC         Note=Probably represents a non-functional splice variant;
CC   -!- SIMILARITY: Belongs to the cyclic nucleotide phosphodiesterase
CC       family.
CC   ---------------------------------------------------------------------
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; L20965; AAA03588.1; -.
DR   EMBL; AF069491; AAC35012.1; -.
DR   EMBL; AF069487; AAC35012.1; JOINED.
DR   EMBL; AF069489; AAC35012.1; JOINED.
DR   EMBL; AF069490; AAC35012.1; JOINED.
DR   EMBL; AF069491; AAC35013.1; -.
DR   EMBL; AF069489; AAC35013.1; JOINED.
DR   EMBL; AF069490; AAC35013.1; JOINED.
DR   EMBL; AF069491; AAC35014.1; -.
DR   EMBL; AF069489; AAC35014.1; JOINED.
DR   EMBL; AF069490; AAC35014.1; JOINED.
DR   EMBL; M37744; AAA69697.1; -.
DR   EMBL; U18087; AAC50458.1; -.
DR   EMBL; U18088; AAA98540.1; -.
DR   EMBL; S75213; AAB33798.1; -.
DR   EMBL; AF069491; AAC35015.1; -.
DR   EMBL; AF069488; AAC35015.1; JOINED.
DR   EMBL; AF069489; AAC35015.1; JOINED.
DR   EMBL; AF069490; AAC35015.1; JOINED.
DR   EMBL; U68532; AAC63832.1; -.
DR   EMBL; U97584; AAC25679.1; -.
DR   EMBL; BC019864; AAH19864.1; -.
DR   PIR; A54442; A54442.
DR   PIR; S55348; S55348.
DR   Genew; HGNC:8780; PDE4A.
DR   MIM; 600126; -.
DR   GO; GO:0005626; C:insoluble fraction; TAS.
DR   GO; GO:0005624; C:membrane fraction; TAS.
DR   GO; GO:0005625; C:soluble fraction; TAS.
DR   GO; GO:0004115; F:cAMP-specific phosphodiesterase activity; TAS.
DR   GO; GO:0007165; P:signal transduction; TAS.
DR   InterPro; IPR003607; Met_phsphohydro.
DR   InterPro; IPR002073; PDEase.
DR   Pfam; PF00233; PDEase; 1.
DR   PRINTS; PR00387; PDIESTERASE1.
DR   SMART; SM00471; HDc; 1.
DR   PROSITE; PS00126; PDEASE_I; 1.
KW   Hydrolase; cAMP; Alternative splicing; Multigene family.
FT   VARSPLIC      1    107       MEPPTVPSERSLSLSLPGPREGQATLKPPPQHLWRQPRTPI
FT                                RIQQRGYSDSAERAERERQPHRPIERADAMDTSDRPGLRTT
FT                                RMSWPSSFHGTGTGSGGAGGGSSRR -> MARPRGLGRIPE
FT                                LQLVAFPVAVAAEDEAFLPEPLAPRAPRRPRSPPSSPVFFA
FT                                SPSPTFRRRLRLLRSCQDLGRQAWAGAG (in isoform
FT                                2).
FT                                /FTId=VSP_004556.
FT   VARSPLIC      1    209       MEPPTVPSERSLSLSLPGPREGQATLKPPPQHLWRQPRTPI
FT                                RIQQRGYSDSAERAERERQPHRPIERADAMDTSDRPGLRTT
FT                                RMSWPSSFHGTGTGSGGAGGGSSRRFEAENGPTPSPGRSPL
FT                                DSQASPGLVLHAGAATSQRRESFLYRSDSDYDMSPKTMSRN
FT                                SSVTSEAHAEDLIVTPFAQVLASLRSVRSNFSLLTNVPVPS
FT                                NKRS -> MCPFPVTTV (in isoform 3).
FT                                /FTId=VSP_004557.
FT   VARSPLIC      1    261       MEPPTVPSERSLSLSLPGPREGQATLKPPPQHLWRQPRTPI
FT                                RIQQRGYSDSAERAERERQPHRPIERADAMDTSDRPGLRTT
FT                                RMSWPSSFHGTGTGSGGAGGGSSRRFEAENGPTPSPGRSPL
FT                                DSQASPGLVLHAGAATSQRRESFLYRSDSDYDMSPKTMSRN
FT                                SSVTSEAHAEDLIVTPFAQVLASLRSVRSNFSLLTNVPVPS
FT                                NKRSPLGGPTPVCKATLSEETCQQLARETLEELDWCLEQLE
FT                                TMQTYRSVSEMASHK -> MPLVDFFCETCSKPWLVGWWDQ
FT                                (in isoform 4).
FT                                /FTId=VSP_004558.
FT   VARSPLIC      1    367       MEPPTVPSERSLSLSLPGPREGQATLKPPPQHLWRQPRTPI
FT                                RIQQRGYSDSAERAERERQPHRPIERADAMDTSDRPGLRTT
FT                                RMSWPSSFHGTGTGSGGAGGGSSRRFEAENGPTPSPGRSPL
FT                                DSQASPGLVLHAGAATSQRRESFLYRSDSDYDMSPKTMSRN
FT                                SSVTSEAHAEDLIVTPFAQVLASLRSVRSNFSLLTNVPVPS
FT                                NKRSPLGGPTPVCKATLSEETCQQLARETLEELDWCLEQLE
FT                                TMQTYRSVSEMASHKFKRMLNRELTHLSEMSRSGNQVSEYI
FT                                STTFLDKQNEVEIPSPTMKEREKQQAPRPRPSQPPPPPVPH
FT                                LQPMSQITGLKKLMHSNSLNNSNIPRFGVKTDQEELLAQ
FT                                -> MVLPSDQGFKLLGNVLQGPEPYRLLTSGLRLHQ (in
FT                                isoform 5).
FT                                /FTId=VSP_004559.
FT   VARSPLIC    644    657       GFIDYIVHPLWETW -> QARGIDGRAQGGFY (in
FT                                isoform 5).
FT                                /FTId=VSP_004560.
FT   VARSPLIC    658    886       Missing (in isoform 5).
FT                                /FTId=VSP_004561.
FT   CONFLICT    736    736       E -> A (IN REF. 1, 2, 6; AAB33798 AND 7).
SQ   SEQUENCE   886 AA;  98201 MW;  483BDF98BA9756CA CRC64;

  Query Match             24.1%;  Score 541;  DB 1;  Length 886;
  Best Local Similarity   32.3%;  Pred. No. 1.6e-36;
  Matches  124;  Conservative   69;  Mismatches  159;  Indels   32;  Gaps    6;

Qy         22 ESERRGSH--PYIDFRIFHSQSEIEVSVSARNIRRLLSFQR-----------YLRSSRF 67
              |  | |:    ||       |:|:|:       |      |           :|:
Db        275 EMSRSGNQVSEYISTTFLDKQNEVEIPSPTMKEREKQQAPRPRPSQPPPPPVPHLQPMSQ 334

Qy         68 FRGTAV---SNSLNI-------LDDDYNGQAKCMLEKVGNWNFDIFLFDRLTNGNSLVSL 117
                |       |||||         :  |         || :  |  :||       | ||  :
Db        335 ITGLKKLMHSNSLNNSNIPRFGVKTDQEELLAQELENLNKWGLNIFCVSDYAGGRSLTCI 394
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Qy        118 TFHLFSLHGLIEYFHLDMMKLRRFLVMIQEDYHSQNPYHNAVHAADVTQAMHCYLKEPKL 177
Db        395 MYMIFQERDLLKKFRIPVDTMVTYMLTLEDHYHADVAYHNSLHAADVLQSTHVLLATPAL 454

Qy        178 ANSVTPWDILLSLIAAATHDLDHPGVNQPFLIKTNHYLATLYKNTSVLENHHWRSAVGLL 237
Db        455 DAVFTDLEILAALFAAAIHDVDHPGVSNQFLINTNSELALMYNDESVLENHHLAVGFKLL 514

Qy        238 RESG--LFSHLPLESRQQMETQIGALILATDISRQNEYLSLFRSHLD------RGDLCLE 289
Db        515 QEDNCDIFQNLSKRQRQSLRKMVIDMVLATDMSKHMTLLADLKTMVETKKVTSSGVLLLD 574

Qy        290 DTRHRHLVLQMALKCADICNPCRTWELSKQWSEKVTEEFFHQGDIEKKYHLGVSPLCDRH 349
Db        575 NYSDRIQVLRNMVHCADLSNPTKPLELYRQWTDRIMAEFFQQGDRERERGMEISPMCDKH 634

Qy        350 TESIANIQIGFMTYLVEPLFTEWA 373
Db        635 TASVEKSQVGFIDYIVHPLWETWA 658
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RESULT 13
CN4D_RAT
ID   CN4D_RAT       STANDARD;      PRT;   672 AA.
AC   P14270;
DT   01-JAN-1990 (Rel. 13, Created)
DT   15-JUL-1998 (Rel. 36, Last sequence update)
DT   10-OCT-2003 (Rel. 42, Last annotation update)
DE   cAMP-specific 3',5'-cyclic phosphodiesterase 4D (EC 3.1.4.17)
DE   (DPDE3).
GN   PDE4D.
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   SEQUENCE FROM N.A. (ISOFORMS 1; 2 AND 3).
RX   MEDLINE=94308045; PubMed=8034568;
RA   Sette C., Vicini E., Conti M.;
RT   "The ratPDE3/IVd phosphodiesterase gene codes for multiple proteins
RT   differentially activated by cAMP-dependent protein kinase.";
RL   J. Biol. Chem. 269:18271-18274(1994).
RN   [2]
RP   REVISION TO 6.
RA   Conti M.;
RL   Submitted (OCT-1997) to the EMBL/GenBank/DDBJ databases.
RN   [3]
RP   SEQUENCE OF 95-672 FROM N.A. (ISOFORM 1).
RX   MEDLINE=95047482; PubMed=7958996;
RA   Bolger G.B., Rodgers L., Riggs M.;
RT   "Differential CNS expression of alternative mRNA isoforms of the
RT   mammalian genes encoding cAMP-specific phosphodiesterases.";
RL   Gene 149:237-244(1994).
RN   [4]
RP   SEQUENCE FROM N.A. (ISOFORMS 2 AND 3).
RC   STRAIN=Wistar;
RX   MEDLINE=94103234; PubMed=8276818;
RA   Monaco L., Vicini E., Conti M.;
RT   "Structure of two rat genes coding for closely related rolipram-
RT   sensitive cAMP phosphodiesterases. Multiple mRNA variants originate
RT   from alternative splicing and multiple start sites.";
RL   J. Biol. Chem. 269:347-357(1994).
RN   [5]
RP   ERRATUM.
RA   Monaco L., Vicini E., Conti M.;
RL   J. Biol. Chem. 269:20806-20806(1994).
RN   [6]
RP   SEQUENCE FROM N.A. (ISOFORM 2).
RC   TISSUE=Testis;
RX   MEDLINE=90046763; PubMed=2554303;
RA   Swinnen J.V., Joseph D.R., Conti M.;
RT   "The mRNA encoding a high-affinity cAMP phosphodiesterase is
RT   regulated by hormones and cAMP.";
RL   Proc. Natl. Acad. Sci. U.S.A. 86:8197-8201(1989).
RN   [7]
RP   SEQUENCE OF 224-672 FROM N.A.
RC   TISSUE=Testis;
RX   MEDLINE=89315790; PubMed=2546153;
RA   Swinnen J.V., Joseph D.R., Conti M.;
RT   "Molecular cloning of rat homologues of the Drosophila melanogaster
RT   dunce cAMP phosphodiesterase: evidence for a family of genes.";
RL   Proc. Natl. Acad. Sci. U.S.A. 86:5325-5329(1989).
CC   -!- CATALYTIC ACTIVITY: Adenosine 3',5'-cyclic phosphate + H(2)O =
CC       adenosine 5'-phosphate.
CC   -!- ENZYME REGULATION: Inhibited by rolipram.
CC   -!- PATHWAY: Cyclic nucleotide metabolism.
CC   -!- ALTERNATIVE PRODUCTS:
CC       Event=Alternative splicing; Named isoforms=3;
CC       Name=1; Synonyms=PDE3.3;
CC         IsoId=P14270-1; Sequence=Displayed;
CC       Name=2; Synonyms=PDE3.1;
CC         IsoId=P14270-2; Sequence=VSP_004581;
CC       Name=3; Synonyms=PDE3.2;
CC         IsoId=P14270-3; Sequence=VSP_004582;
CC   -!- PTM: Isoform 1 is rapidly activated by PKA through
CC       phosphorylation.
CC   -!- SIMILARITY: Belongs to the cyclic nucleotide phosphodiesterase
CC       family.
CC   ---------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; U09457; AAB81869.1; -.
DR   EMBL; U09456; AAA20393.1; -.
DR   EMBL; L27059; AAA56857.1; -.
DR   EMBL; U01280; AAA18925.1; -.
DR   EMBL; U01278; AAA18925.1; JOINED.
DR   EMBL; U01282; AAA18925.1; JOINED.
DR   EMBL; U01283; AAA18925.1; JOINED.
DR   EMBL; U01284; AAA18925.1; JOINED.
DR   EMBL; U01285; AAA18925.1; JOINED.
DR   EMBL; U01286; AAA18925.1; JOINED.
DR   EMBL; U01287; AAA18925.1; JOINED.
DR   EMBL; U01279; AAA18925.1; JOINED.
DR   EMBL; U01280; AAA18924.1; -.
DR   EMBL; U01278; AAA18924.1; JOINED.
DR   EMBL; U01282; AAA18924.1; JOINED.
DR   EMBL; U01283; AAA18924.1; JOINED.
DR   EMBL; U01284; AAA18924.1; JOINED.
DR   EMBL; U01285; AAA18924.1; JOINED.
DR   EMBL; U01286; AAA18924.1; JOINED.
DR   EMBL; U01287; AAA18924.1; JOINED.
DR   EMBL; U01279; AAA18924.1; JOINED.
DR   EMBL; U09455; AAA20401.1; -.
DR   EMBL; L27060; AAC26969.1; -.
DR   PIR; B53109; B53109.
DR   InterPro; IPR003607; Met_phsphohydro.
DR   InterPro; IPR002073; PDEase.
DR   Pfam; PF00233; PDEase; 1.
DR   PRINTS; PR00387; PDIESTERASE1.
DR   SMART; SM00471; HDc; 1.
DR   PROSITE; PS00126; PDEASE_I; 1.
KW   Hydrolase; cAMP; Alternative splicing; Multigene family;
KW   Phosphorylation.
FT   VARSPLIC      1    133       MMHVNTFPFRRHSWICFDVDNGTSAGRSPLDPMTSPGSGLI
FT                                LQANFVHSQRRESFLYRSDSDYDLSPKSMSRNSSIASDIHG
FT                                DDLIVTPFAQVLASLRTVRNNFAALTNLQDRAPSKRSPMCN
FT                                QPSINKATIT -> MKEQPSCAGTGHPSMAGYGRMAPFELA
FT                                GGPVKRLRTESPFPCLFA (in isoform 2).
FT                                /FTId=VSP_004581.
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FT   VARSPLIC      1    167       Missing (in isoform 3).
FT                                /FTId=VSP_004582.
FT   CONFLICT     95     95       A -> N (IN REF. 3).
FT   CONFLICT    349    355       MISSING (IN REF. 4).
FT   CONFLICT    510    510       G -> E (IN REF. 3).
FT   CONFLICT    626    626       C -> Y (IN REF. 3).
SQ   SEQUENCE   672 AA;  76263 MW;  63CE38FA654A0BDD CRC64;

  Query Match             24.0%;  Score 539;  DB 1;  Length 672;
  Best Local Similarity   31.6%;  Pred. No. 1.6e-36;
  Matches  122;  Conservative   81;  Mismatches  151;  Indels   32;  Gaps    7;

Qy          8 RMLGDVRVRSRAGFESERRGSHPYIDFRIFHSQSEIEV--------SVSARNIRRLLSFQ 59
              | |  :   ||:| :      |: ::|      | |:|:           | : ::   :
Db        178 RELTHLSEMSRSGNQVSEYISNTFLD-----KQHEVEIPSPTQKEKEKKKRPMSQISGVK 232

Qy         60 RYLRSSRFFRGTAVSNS----LNILDDDYNGQAKCMLEKVGNWNFDIFLFDRLTNGNSLV 115
              : : ||      :::||      :  :  :  ||  || |  |    :|    |:    |
Db        233 KLMHSS------SLTNSCIPRFGVKTEQEDVLAK-ELEDVNKWGLHVFRIAELSGNRPLT 285

Qy        116 SLTFHLFSLHGLIEYFHLDMMKLRRFLVMIQEDYHSQNPYHNAVHAADVTQAMHCYLKEP 175
               :   :|    |:: | : :  |  :|: ::: ||:   ||| :||||| |: |  |  |
Db        286 VIMHTIFQERDLLKTFKIPVDTLITYLMTLEDHYHADVAYHNNIHAADVVQSTHVLLSTP 345

Qy        176 KLANSVTPWDILLSLIAAATHDLDHPGVNQPFLIKTNHYLATLYKNTSVLENHHWRSAVG 235
               |    |  :|| :: |:| ||:|||||:  ||| ||  || :| ::|||||||
Db        346 ALEAVFTDLEILAAIFASAIHDVDHPGVSNQFLINTNSELALMYNDSSVLENHHLAVGFK 405

Qy        236 LLRESG--LFSHLPLESRQQMETQIGALILATDISRQNEYLSLFRSHLD------RGDLC 287
              ||:|    :| :|  : || :      ::||||:|:    |:  :: ::        | |
Db        406 LLQEENCDIFQNLTKKQRQSLRKMAIDIVLATDMSKHMNLLADLKTMVETKKVTSSGVLL 465

Qy        288 LEDTRHRHLVLQMALKCADICNPCRTWELSKQWSEKVTEEFFHQGDIEKKYHLGVSPLCD 347
              |::   |  |||  : |||: || :  :| :||:::: |||| ||| |::  : :||:||
Db        466 LDNYSDRIQVLQNMVHCADLSNPTKPLQLYRQWTDRIMEEFFRQGDRERERGMEISPMCD 525

Qy        348 RHTESIANIQIGFMTYLVEPLFTEWA 373
              :|  |:   |:||: |:| ||:  ||
Db        526 KHNASVEKSQVGFIDYIVHPLWETWA 551


RESULT 14
CN4C_RAT
ID   CN4C_RAT       STANDARD;      PRT;   536 AA.
AC   P14644;
DT   01-APR-1990 (Rel. 14, Created)
DT   01-OCT-1996 (Rel. 34, Last sequence update)
DT   28-FEB-2003 (Rel. 41, Last annotation update)
DE   cAMP-specific 3',5'-cyclic phosphodiesterase 4C (EC 3.1.4.17)
DE   (DPDE1) (Fragment).
GN   PDE4C.
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=95047482; PubMed=7958996;
RA   Bolger G.B., Rodgers L., Riggs M.;
RT   "Differential CNS expression of alternative mRNA isoforms of the
RT   mammalian genes encoding cAMP-specific phosphodiesterases.";
RL   Gene 149:237-244(1994).
RN   [2]
RP   SEQUENCE OF 153-511 FROM N.A.
RC   TISSUE=Testis;
RX   MEDLINE=89315790; PubMed=2546153;
RA   Swinnen J.V., Joseph D.R., Conti M.;
RT   "Molecular cloning of rat homologues of the Drosophila melanogaster
RT   dunce cAMP phosphodiesterase: evidence for a family of genes.";
RL   Proc. Natl. Acad. Sci. U.S.A. 86:5325-5329(1989).
CC   -!- CATALYTIC ACTIVITY: Adenosine 3',5'-cyclic phosphate + H(2)O =
CC       adenosine 5'-phosphate.
CC   -!- ENZYME REGULATION: Inhibited by rolipram.
CC   -!- PATHWAY: Cyclic nucleotide metabolism.
CC   -!- SIMILARITY: Belongs to the cyclic nucleotide phosphodiesterase
CC       family.
CC   ---------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; L27061; AAA56858.1; -.
DR   EMBL; M25347; AAA41847.1; -.
DR   PIR; I67945; I67945.
DR   InterPro; IPR003607; Met_phsphohydro.
DR   InterPro; IPR002073; PDEase.
DR   Pfam; PF00233; PDEase; 1.
DR   PRINTS; PR00387; PDIESTERASE1.
DR   SMART; SM00471; HDc; 1.
DR   PROSITE; PS00126; PDEASE_I; 1.
KW   Hydrolase; cAMP; Multigene family.
FT   NON_TER       1      1
FT   DOMAIN      524    534       POLY-GLU.
FT   CONFLICT    218    218       R -> S (IN REF. 2).
FT   CONFLICT    507    507       S -> N (IN REF. 2).
SQ   SEQUENCE   536 AA;  60063 MW;  87D12BE2C46642F3 CRC64;

  Query Match             23.8%;  Score 534.5;  DB 1;  Length 536;
  Best Local Similarity   32.2%;  Pred. No. 2.8e-36;
  Matches  118;  Conservative   71;  Mismatches  159;  Indels   19;  Gaps    6;

Qy         22 ESERRGSH--PYIDFRIFHSQSEIEVSVSARN-----IRRLLSFQRYLRSSRFFRGTAVS 74
              |: | |:    ||        |:|:|:          : ::   ::   :|     ||
Db        117 ETSRSGNQVSEYISQTFLDQQAEVELPAPPTEDHPWPMAQITGLRKSCHTS---LPTAAI 173

Qy         75 NSLNILDDDYNGQAKCMLEKVGNWNFDIFLFDRLTNGNSLVSLTFHLFSLHGLIEYFHLD 134
                 :  |     ||  ||    |  |:|    |:    | :: | :    |:: | :
Db        174 PRFGVQTDQEEQLAK-ELEDTNKWGLDVFKVAELSGNRPLTAVIFRVLQERDLLKTFQIP 232

Qy        135 MMKLRRFLVMIQEDYHSQNPYHNAVHAADVTQAMHCYLKEPKLANSVTPWDILLSLIAAA 194
                 | |:|: ::  |||   |||::|||||  |: |  |  | |     |  ::| :: | |
Db        233 ADTLLRYLLTLEGHYHSNVAYHNSIHAADVVQSAHVLLGTPALEAVFTDLEVLAAIFACA 292

Qy        195 THDLDHPGVNQPFLIKTNHYLATLYKNTSVLENHHWRSAVGLLR--ESGLFSHLPLESRQ 252
              ||:|||||:  ||| ||  || :| ::|||||||       ||:     :| :|  : :
Db        293 IHDVDHPGVSNQFLINTNSELALMYNDSSVLENHHLAVGFKLLQGENCDIFQNLSTKQKL 352

Qy        253 QMETQIGALILATDISRQNEYLSLFRSHLDR------GDLCLEDTRHRHLVLQMALKCAD 306
               :   :  ::||||:|:    |:  :: ::       | | |::  |  |||  : |||
Db        353 SLRRMVIDMVLATDMSKHMSLLADLKTMVETKKVTSLGVLLLDNYSDRIQVLQSLVHCAD 412

Qy        307 ICNPCRTWELSKQWSEKVTEEFFHQGDIEKKYHLGVSPLCDRHTESIANIQIGFMTYLVE 366
              : || :   | :||:|::  ||| ||| |::  | :||:||:|| |:   |:||: |:
Db        413 LSNPAKPLPLYRQWTERIMAEFFQQGDRERESGLDISPMCDKHTASVEKSQVGFIDYIAH 472

Qy        367 PLFTEWA 373
              ||:  ||
Db        473 PLWETWA 479


RESULT 15
CN8A_HUMAN
ID   CN8A_HUMAN     STANDARD;      PRT;   829 AA.
AC   O60658; Q969I1; Q96PC9; Q96PD0; Q96PD1; Q9UMB7;
DT   15-JUL-1999 (Rel. 38, Created)
DT   28-FEB-2003 (Rel. 41, Last sequence update)
DT   15-MAR-2004 (Rel. 43, Last annotation update)
DE   High-affinity cAMP-specific and IBMX-insensitive 3',5'-cyclic
DE   phosphodiesterase 8A (EC 3.1.4.17).
GN   PDE8A.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
```

```
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A. (ISOFORMS 1; 2; 3 AND 4-5).
RC   TISSUE=Testis;
RX   MEDLINE=21601118; PubMed=11738832;
RA   Wang P., Wu P., Egan R.W., Billah M.M.;
RT   "Human phosphodiesterase 8A splice variants: cloning, gene
RT   organization, and tissue distribution.";
RL   Gene 280:183-194(2001).
RN   [2]
RP   SEQUENCE OF 117-829 FROM N.A. (ISOFORMS 1 AND 2).
RX   MEDLINE=98289571; PubMed=9618252;
RA   Fisher D.A., Smith J.F., Pillar J.S., St Denis S.H., Cheng J.B.;
RT   "Isolation and characterization of PDE8A, a novel human cAMP-specific
RT   phosphodiesterase.";
RL   Biochem. Biophys. Res. Commun. 246:570-577(1998).
RN   [3]
RP   SEQUENCE OF 670-829 FROM N.A.
RA   Carim L., Estivill X., Sumoy L., Escarceller M.;
RL   Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.
CC   -!- FUNCTION: Plays a role in signal transduction by regulating the
CC       intracellular concentration of cyclic nucleotides. This
CC       phosphodiesterase, which has a high affinity for cAMP, may be
CC       involved in maintaining basal levels of the cyclic nucleotide
CC       and/or in the cAMP regulation of germ cell development.
CC   -!- CATALYTIC ACTIVITY: Adenosine 3',5'-cyclic phosphate + H(2)O =
CC       adenosine 5'-phosphate.
CC   -!- COFACTOR: Requires divalent cations. Magnesium or manganese are
CC       required for maximum activity, in vitro.
CC   -!- ENZYME REGULATION: Inhibited by dipyridimole. Insensitive to
CC       selective PDE inhibitors including rolipram and zaprinast as well
CC       as to the non-selective inhibitor, IBMX. Unaffected by cGMP.
CC   -!- PATHWAY: Cyclic nucleotide metabolism.
CC   -!- ALTERNATIVE PRODUCTS:
CC       Event=Alternative splicing; Named isoforms=4;
CC       Name=1; Synonyms=PDE8A1;
CC         IsoId=O60658-1; Sequence=Displayed;
CC       Name=2; Synonyms=PDE8A2;
CC         IsoId=O60658-2; Sequence=VSP_004597;
CC       Name=3; Synonyms=PDE8A3;
CC         IsoId=O60658-3; Sequence=VSP_004596;
CC       Name=4-5; Synonyms=PDE8A4, PDE8A5;
CC         IsoId=O60658-4; Sequence=VSP_004595;
CC   -!- TISSUE SPECIFICITY: Expressed in most tissues except thymus and
CC       peripheral blood Leukocytes. Highest levels in testis, ovary,
CC       small intestine and colon.
CC   -!- DOMAIN: Composed of a C-terminal catalytic domain containing two
CC       putative divalent metal sites and an N-terminal regulatory domain.
CC   -!- SIMILARITY: Belongs to the cyclic nucleotide phosphodiesterase
CC       family.
CC   -!- SIMILARITY: Contains 1 PAS (PER-ARNT-SIM) dimerization domain.
CC   -!- SIMILARITY: Contains 1 PAS-associated C-terminal (PAC) domain.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; AF388183; AAL18610.1; -.
DR   EMBL; AF388184; AAL18611.1; -.
DR   EMBL; AF388185; AAL18612.1; -.
DR   EMBL; AF388186; AAL18613.1; -.
DR   EMBL; AF388187; AAL18614.1; -.
DR   EMBL; AF056490; AAC39763.1; -.
DR   EMBL; AL109687; CAB52020.1; -.
DR   PIR; JW0088; JW0088.
DR   Genew; HGNC:8793; PDE8A.
DR   MIM; 602972; -.
DR   GO; GO:0004114; F:3',5'-cyclic-nucleotide phosphodiesterase a. . .; NAS.
DR   GO; GO:0009187; P:cyclic nucleotide metabolism; NAS.
DR   InterPro; IPR003607; Met_phsphohydro.
DR   InterPro; IPR000014; PAS_domain.
DR   InterPro; IPR002073; PDEase.
DR   Pfam; PF00989; PAS; 1.
DR   Pfam; PF00233; PDEase; 1.
DR   PRINTS; PR00387; PDIESTERASE1.
DR   SMART; SM00471; HDc; 1.
DR   SMART; SM00091; PAS; 1.
DR   TIGRFAMs; TIGR00229; sensory_box; 1.
DR   PROSITE; PS00126; PDEASE_I; 1.
DR   PROSITE; PS50112; PAS; 1.
KW   Hydrolase; cAMP; Alternative splicing; Manganese; Magnesium;
KW   Multigene family.
FT   DOMAIN      213    283       PAS.
FT   DOMAIN      287    329       PAC.
FT   DOMAIN      531    813       CATALYTIC (BY SIMILARITY).
FT   METAL       556    556       MAGNESIUM OR MANGANESE 1 (POTENTIAL).
FT   METAL       560    560       MAGNESIUM OR MANGANESE 1 (POTENTIAL).
FT   METAL       585    585       MAGNESIUM OR MANGANESE 1 (POTENTIAL).
FT   METAL       596    596       MAGNESIUM OR MANGANESE 2 (POTENTIAL).
FT   METAL       600    600       MAGNESIUM OR MANGANESE 2 (POTENTIAL).
FT   METAL       626    626       MAGNESIUM OR MANGANESE 2 (POTENTIAL).
FT   VARSPLIC      1    247       Missing (in isoform 4-5).
FT                                /FTId=VSP_004595.
FT   VARSPLIC      1    380       Missing (in isoform 3).
FT                                /FTId=VSP_004596.
FT   VARSPLIC    239    284       Missing (in isoform 2).
FT                                /FTId=VSP_004597.
FT   CONFLICT    344    344       H -> R (IN REF. 2).
FT   CONFLICT    399    399       I -> V (IN REF. 2).
SQ   SEQUENCE   829 AA;  93303 MW;  99BD05EA185A42CD CRC64;

  Query Match           22.4%;  Score 503;  DB 1;  Length 829;
  Best Local Similarity  31.6%;  Pred. No. 1.9e-33;
  Matches  117;  Conservative   76;  Mismatches  145;  Indels   32;  Gaps    7;

Qy        54 RLLSFQRYLRSSRFFRGTAVSNSLNILD----DDYNGQAKCMLEKVGNWNFDIFLFDRLT 109
             | ||   |: |:   : | : :| ||:     ||   :    :|    |:|||  :  |
Db       454 RRLSGNEYVLST---KNTQMVSS-NIITPISLDDVPPRIARAMENEEYWDFDIFELEAAT 509

Qy       110 NGNSLVSLTFHLFSLHGLIEYFHLDMMKLRRFLVMIQEDYHSQNPYHNAVHAADVTQAMH 169
             :  |: |   :|:  |: |: |     || :| :|: :||| |||||: |:|||  |
Db       510 HNRPLIYLGLKMFARFGICEFLHCSESTLRSWLQIIEANYHSSNPYHNSTHSADVLHATA 569

Qy       170 CYLKEPKLANSVTPWDILLSLIAAATHDLDHPGVNQPFLIKTNHYLATLYKNTSVLENHH 229
             :| : ::  :: | | : :|||| ||:|||     ||       || || :|:|||:||
Db       570 YFLSKERIKETLDPIDEVAALIAATIHDVDHPGRTNSFLCNAGSELAILYNDTAVLESHH 629

Qy       230 WRSAVGLLR---ESGLFSHLPLESRQQMETQIGALILATDISRQNEYLSLFRSHLDRGDL 286
             | |     :  :| ::     : :   |  ::|||:::: |::: | : :::
Db       630 AALAFQLTTGDDKCNIFKNMERNDYRTLRQGIIDMVLATEMTKHFEHVNKFVNSINKPLA 689

Qy       287 CLEDT----------------RHRHLVLQMALKCADICNPCRTWELSKQWSEKVTEEFF 329
             ||:              :| |: :| :|||: |||| :   :|: :::||:|
Db       690 TLEENGETDKNQEVINTMLRTPENRTLIKRMLIKCADVSNPCRPLQYCIEWAARISEEYF 749

Qy       330 HQGDIEKKYHLG-VSPLCDRHTESIANIQIGFMTYLVEPLFTEWARFSNTRLSQTMLGHV 388
             | | ||:  |  | |: ||:| ||    || |: | :  :|  |  | :      :: |:
Db       750 SQTDEEKQQGLPVVMPVFDRNTCSIPKSQISFIDYFITDMFDAWDAFVDL---PDLMQHL 806

Qy       389 GLNKASWKGL 398
               |  ||||
Db       807 DNNFKYWKGL 816


Search completed: May 26, 2004, 09:25:02
Job time : 19 secs
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GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: May 26, 2004, 09:26:43 ; Search time 577 Seconds
(without alignments)
205.928 Million cell updates/sec

Title: US-09-966-781A-1
Perfect score: 2243
Sequence: 1 DQTALYIRMLGDVRVRSRAG.....DTDAAFELNSQLLPQENRLS 426

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1149313 seqs, 278921704 residues

Total number of hits satisfying chosen parameters: 1149313

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_AA:*
1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*
2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*
3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*
4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep:*
5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep:*
6: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep:*
7: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep:*
8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
9: /cgn2_6/ptodata/1/pubpaa/US09A_PUBCOMB.pep:*
10: /cgn2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pep:*
11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep:*
12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep:*
13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*
14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*
15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep:*
16: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep:*
17: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep:*
18: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	2243	100.0	426	10	US-09-966-781A-1	Sequence 1, Appli
2	2116	94.3	426	10	US-09-966-781A-3	Sequence 3, Appli
3	2105	93.8	426	10	US-09-966-781A-2	Sequence 2, Appli
4	1903	84.8	432	9	US-09-764-898-208	Sequence 208, App
5	1787	79.7	336	14	US-10-258-746-2	Sequence 2, Appli
6	1383.5	61.7	502	12	US-10-311-104-1	Sequence 1, Appli
7	1383.5	61.7	502	14	US-10-273-517-1	Sequence 1, Appli
8	1383.5	61.7	502	15	US-10-386-414-4	Sequence 4, Appli
9	1079	48.1	211	9	US-09-764-898-280	Sequence 280, App
10	1079	48.1	211	10	US-09-989-442-120	Sequence 120, App
11	871	38.8	320	15	US-10-386-414-6	Sequence 6, Appli
12	555	24.7	610	14	US-10-272-970-17	Sequence 17, Appl
13	555	24.7	610	15	US-10-627-929-9	Sequence 9, Appli
14	551	24.6	721	12	US-09-983-754-2	Sequence 2, Appli
15	550	24.5	517	16	US-10-442-675-2	Sequence 2, Appli
16	550	24.5	564	9	US-09-947-305-2	Sequence 2, Appli
17	550	24.5	564	12	US-09-983-754-4	Sequence 4, Appli
18	550	24.5	564	14	US-10-076-597-48	Sequence 48, Appl
19	550	24.5	564	14	US-10-205-219-19	Sequence 19, Appl
20	550	24.5	564	15	US-10-149-536-8	Sequence 8, Appli
21	550	24.5	657	12	US-10-087-192-1629	Sequence 1629, Ap
22	550	24.5	659	15	US-10-149-536-2	Sequence 2, Appli
23	550	24.5	721	12	US-10-087-192-1632	Sequence 1632, Ap
24	550	24.5	721	15	US-10-149-536-9	Sequence 9, Appli
25	550	24.5	736	15	US-10-149-536-6	Sequence 6, Appli
26	550	24.5	736	15	US-10-149-536-7	Sequence 7, Appli
27	544	24.3	1124	14	US-10-257-909A-6	Sequence 6, Appli
28	542	24.2	507	14	US-10-076-597-49	Sequence 49, Appl
29	542	24.2	507	14	US-10-067-514-10	Sequence 10, Appl
30	542	24.2	507	15	US-10-419-723-10	Sequence 10, Appl
31	542	24.2	517	12	US-10-165-135-6	Sequence 6, Appli
32	542	24.2	517	12	US-10-703-939-6	Sequence 6, Appli
33	542	24.2	517	12	US-10-704-447-6	Sequence 6, Appli
34	542	24.2	564	12	US-10-165-135-5	Sequence 5, Appli
35	542	24.2	564	12	US-10-703-939-5	Sequence 5, Appli
36	542	24.2	564	12	US-10-704-447-5	Sequence 5, Appli
37	542	24.2	585	14	US-10-067-514-9	Sequence 9, Appli
38	542	24.2	585	15	US-10-419-723-9	Sequence 9, Appli
39	542	24.2	673	14	US-10-076-597-51	Sequence 51, Appl
40	542	24.2	673	14	US-10-067-514-6	Sequence 6, Appli
41	542	24.2	673	15	US-10-419-723-6	Sequence 6, Appli
42	542	24.2	673	16	US-10-239-439-4	Sequence 4, Appli
43	542	24.2	687	14	US-10-067-514-8	Sequence 8, Appli
44	542	24.2	687	15	US-10-419-723-8	Sequence 8, Appli
45	542	24.2	721	12	US-10-165-135-4	Sequence 4, Appli

ALIGNMENTS

RESULT 1
US-09-966-781A-1
; Sequence 1, Application US/09966781A
; Publication No. US20030036184A1
; GENERAL INFORMATION:
; APPLICANT: SOULARD, PATRICIA
; TITLE OF INVENTION: POLYPEPTIDES EXHIBITING PDE7 ACTIVITY AND THEIR USE FOR
; TITLE OF INVENTION: SELECTING COMPOUNDS WHICH INHIBIT PDE7 ENZYME ACTIVITY
; FILE REFERENCE: A0000281US
; CURRENT APPLICATION NUMBER: US/09/966,781A
; CURRENT FILING DATE: 2001-09-28
; PRIOR APPLICATION NUMBER: EP004026837
; PRIOR FILING DATE: 2000-09-28
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 426
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-966-781A-1

Query Match 100.0%; Score 2243; DB 10; Length 426;
Best Local Similarity 100.0%; Pred. No. 3.1e-225;
Matches 426; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 DQTALYIRMLGDVRVRSRAGFESERRGSHPYIDFRIFHSQSEIEVSVSARNIRRLLSFQR 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 DQTALYIRMLGDVRVRSRAGFESERRGSHPYIDFRIFHSQSEIEVSVSARNIRRLLSFQR 60

Qy         61 YLRSSRFFRGTAVSNSLNILDDDYNGQAKCMLEKVGNWNFDIFLFDRLTNGNSLVSLTFH 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 YLRSSRFFRGTAVSNSLNILDDDYNGQAKCMLEKVGNWNFDIFLFDRLTNGNSLVSLTFH 120

Qy        121 LFSLHGLIEYFHLDMMKLRRFLVMIQEDYHSQNPYHNAVHAADVTQAMHCYLKEPKLANS 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 LFSLHGLIEYFHLDMMKLRRFLVMIQEDYHSQNPYHNAVHAADVTQAMHCYLKEPKLANS 180

Qy        181 VTPWDILLSLIAAATHDLDHPGVNQPFLIKTNHYLATLYKNTSVLENHHWRSAVGLLRES 240
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Db        181 VTPWDILLSLIAAATHDLDHPGVNQPFLIKTNHYLATLYKNTSVLENHHWRSAVGLLRES 240

Qy        241 GLFSHLPLESRQQMETQIGALILATDISRQNEYLSLFRSHLDRGDLCLEDTRHRHLVLQM 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GLFSHLPLESRQQMETQIGALILATDISRQNEYLSLFRSHLDRGDLCLEDTRHRHLVLQM 300

Qy        301 ALKCADICNPCRTWELSKQWSEKVTEEFFHQGDIEKKYHLGVSPLCDRHTESIANIQIGF 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 ALKCADICNPCRTWELSKQWSEKVTEEFFHQGDIEKKYHLGVSPLCDRHTESIANIQIGF 360

Qy        361 MTYLVEPLFTEWARFSNTRLSQTMLGHVGLNKASWKGLQREQSSSEDTDAAFELNSQLLP 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 MTYLVEPLFTEWARFSNTRLSQTMLGHVGLNKASWKGLQREQSSSEDTDAAFELNSQLLP 420

Qy        421 QENRLS 426
              ||||||
Db        421 QENRLS 426
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RESULT 2
US-09-966-781A-3
; Sequence 3, Application US/09966781A
; Publication No. US20030036184A1
; GENERAL INFORMATION:
; APPLICANT: SOULARD, PATRICIA
; TITLE OF INVENTION: POLYPEPTIDES EXHIBITING PDE7 ACTIVITY AND THEIR USE FOR
; TITLE OF INVENTION: SELECTING COMPOUNDS WHICH INHIBIT PDE7 ENZYME ACTIVITY
; FILE REFERENCE: A0000281US
; CURRENT APPLICATION NUMBER: US/09/966,781A
; CURRENT FILING DATE: 2001-09-28
; PRIOR APPLICATION NUMBER: EP004026837
; PRIOR FILING DATE: 2000-09-28
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 426
; TYPE: PRT
; ORGANISM: Rattus sp.
US-09-966-781A-3

Query Match 94.3%; Score 2116; DB 10; Length 426;
Best Local Similarity 94.1%; Pred. No. 5.8e-212;
Matches 401; Conservative 9; Mismatches 16; Indels 0; Gaps 0;

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              ||||||||||||||||||||:||||||||||||||:||||| ||||||||||||||||||
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Qy         61 YLRSSRFFRGTAVSNSLNILDDDYNGQAKCMLEKVGNWNFDIFLFDRLTNGNSLVSLTFH 120
              |||||||||| | |||||:|||||||||||||||||||||||||||||||||||||||||
Db         61 YLRSSRFFRGATVCRSLNILDEDYNGQAKCMLEKVGNWNFDIFLFDRLTNGNSLVSLTFH 120

Qy        121 LFSLHGLIEYFHLDMMKLRRFLVMIQEDYHSQNPYHNAVHAADVTQAMHCYLKEPKLANS 180
              |||||||||||||:||||||||||||||||||||||||||||||||||||||||||||||
Db        121 LFSLHGLIEYFHLDMVKLRRFLVMIQEDYHSQNPYHNAVHAADVTQAMHCYLKEPKLANS 180

Qy        181 VTPWDILLSLIAAATHDLDHPGVNQPFLIKTNHYLATLYKNTSVLENHHWRSAVGLLRES 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 VTPWDILLSLIAAATHDLDHPGVNQPFLIKTNHYLATLYKNTSVLENHHWRSAVGLLRES 240

Qy        241 GLFSHLPLESRQQMETQIGALILATDISRQNEYLSLFRSHLDRGDLCLEDTRHRHLVLQM 300
              |||||||||||| :|| |||||||||||||||||||||||:||| |:| ||||||||||
Db        241 GLFSHLPLESRHEMEAQIGALILATDISRQNEYLSLFRSHLDKGDLHLDDGRHRHLVLQM 300

Qy        301 ALKCADICNPCRTWELSKQWSEKVTEEFFHQGDIEKKYHLGVSPLCDRHTESIANIQIGF 360
              |||||||||||| |||||||||||||||||||||||||||||||| ||||||||||||
Db        301 ALKCADICNPCRNWELSKQWSEKVTEEFFHQGDIEKKYHLGVSPLCDRQTESIANIQIGF 360

Qy        361 MTYLVEPLFTEWARFSNTRLSQTMLGHVGLNKASWKGLQREQSSSEDTDAAFELNSQLLP 420
              |||| ||||||||||:||||||||||||||||||||:| ||||  ||||||||||
Db        361 MTYLQEPLFTEWARFSDTRLSQTMLGHVGLNKASWKGLQRQQPSSEDASAAFELNSQLLT 420
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Qy        421 QENRLS 426
              ||||||
Db        421 QENRLS 426
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RESULT 3
US-09-966-781A-2
; Sequence 2, Application US/09966781A
; Publication No. US20030036184A1
; GENERAL INFORMATION:
; APPLICANT: SOULARD, PATRICIA
; TITLE OF INVENTION: POLYPEPTIDES EXHIBITING PDE7 ACTIVITY AND THEIR USE FOR
; TITLE OF INVENTION: SELECTING COMPOUNDS WHICH INHIBIT PDE7 ENZYME ACTIVITY
; FILE REFERENCE: A0000281US
; CURRENT APPLICATION NUMBER: US/09/966,781A
; CURRENT FILING DATE: 2001-09-28
; PRIOR APPLICATION NUMBER: EP004026837
; PRIOR FILING DATE: 2000-09-28
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 426
; TYPE: PRT
; ORGANISM: Mus sp.
US-09-966-781A-2

Query Match 93.8%; Score 2105; DB 10; Length 426;
Best Local Similarity 93.7%; Pred. No. 8.2e-211;
Matches 399; Conservative 13; Mismatches 14; Indels 0; Gaps 0;

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Db          1 DQTALYIRMLGDVRVRSRAGFETERRGSHPYIDFRIFHSQSDIEASVSARNIRRLLSFQR 60

Qy         61 YLRSSRFFRGTAVSNSLNILDDDYNGQAKCMLEKVGNWNFDIFLFDRLTNGNSLVSLTFH 120
              |||||| ||| | :||:|||:|||||||||||||||||||||||||||||||||||||
Db         61 YLRSSRVFRGATVCSSLDILDEDYNGQAKCMLEKVGNWNFDIFLFDRLTNGNSLVSLTFH 120

Qy        121 LFSLHGLIEYFHLDMMKLRRFLVMIQEDYHSQNPYHNAVHAADVTQAMHCYLKEPKLANS 180
              |||||||||||||:|||||||||||||||||||||||||||||||||||||||||||:|
Db        121 LFSLHGLIEYFHLDMVKLRRFLVMIQEDYHSQNPYHNAVHAADVTQAMHCYLKEPKLASS 180

Qy        181 VTPWDILLSLIAAATHDLDHPGVNQPFLIKTNHYLATLYKNTSVLENHHWRSAVGLLRES 240
              ||||||||||||||||||||||||||||||||||||||||||||:|||||||||||||||
Db        181 VTPWDILLSLIAAATHDLDHPGVNQPFLIKTNHYLATLYKNSSVLENHHWRSAVGLLRES 240

Qy        241 GLFSHLPLESRQQMETQIGALILATDISRQNEYLSLFRSHLDRGDLCLEDTRHRHLVLQM 300
              |||||||||||:|| ||||||||||||||||||||||||:||| |:| ||||||||||
Db        241 GLFSHLPLESRQEMEAQIGALILATDISRQNEYLSLFRSHLDKGDLHLDDGRHRHLVLQM 300

Qy        301 ALKCADICNPCRTWELSKQWSEKVTEEFFHQGDIEKKYHLGVSPLCDRHTESIANIQIGF 360
              |||||||||||| |||||||||||||||||||||||||||||||| ||||||||||||
Db        301 ALKCADICNPCRNWELSKQWSEKVTEEFFHQGDIEKKYHLGVSPLCDRQTESIANIQIGF 360

Qy        361 MTYLVEPLFTEWARFSNTRLSQTMLGHVGLNKASWKGLQRQQPSSEDANAAFELNSQLLT 420
              |||||||||||||| |||||||||||||||||||||:| |||| :||||||||||
Db        361 MTYLVEPLFTEWARFSATRLSQTMLGHVGLNKASWKGLQRQQPSSEDANAAFELNSQLLT 420
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Qy        421 QENRLS 426
              ||||||
Db        421 QENRLS 426
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RESULT 4
US-09-764-898-208
; Sequence 208, Application US/09764898
; Patent No. US20020090673A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PJZ01
; CURRENT APPLICATION NUMBER: US/09/764,898
; CURRENT FILING DATE: 2001-01-17

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;  Prior application data removed - consult PALM or file wrapper
;  NUMBER OF SEQ ID NOS: 311
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 208
;    LENGTH: 432
;    TYPE: PRT
;    ORGANISM: Homo sapiens
;    FEATURE:
;    NAME/KEY: SITE
;    LOCATION: (419)
;    OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-764-898-208

  Query Match             84.8%;  Score 1903;  DB 9;  Length 432;
  Best Local Similarity   99.2%;  Pred. No. 1.1e-189;
  Matches  361;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 DQTALYIRMLGDVRVRSRAGFESERRGSHPYIDFRIFHSQSEIEVSVSARNIRRLLSFQR 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         65 DQTALYIRMLGDVRVRSRAGFESERRGSHPYIDFRIFHSQSEIEVSVSARNIRRLLSFQR 124

Qy         61 YLRSSRFFRGTAVSNSLNILDDDYNGQAKCMLEKVGNWNFDIFLFDRLTNGNSLVSLTFH 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        125 YLRSSRFFRGTAVSNSLNILDDDYNGQAKCMLEKVGNWNFDIFLFDRLTNGNSLVSLTFH 184

Qy        121 LFSLHGLIEYFHLDMMKLRRFLVMIQEDYHSQNPYHNAVHAADVTQAMHCYLKEPKLANS 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        185 LFSLHGLIEYFHLDMMKLRRFLVMIQEDYHSQNPYHNAVHAADVTQAMHCYLKEPKLANS 244

Qy        181 VTPWDILLSLIAAATHDLDHPGVNQPFLIKTNHYLATLYKNTSVLENHHWRSAVGLLRES 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        245 VTPWDILLSLIAAATHDLDHPGVNQPFLIKTNHYLATLYKNTSVLENHHWRSAVGLLRES 304

Qy        241 GLFSHLPLESRQQMETQIGALILATDISRQNEYLSLFRSHLDRGDLCLEDTRHRHLVLQM 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        305 GLFSHLPLESRQQMETQIGALILATDISRQNEYLSLFRSHLDRGDLCLEDTRHRHLVLQM 364

Qy        301 ALKCADICNPCRTWELSKQWSEKVTEEFFHQGDIEKKYHLGVSPLCDRHTESIANIQIGF 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||| ||||
Db        365 ALKCADICNPCRTWELSKQWSEKVTEEFFHQGDIEKKYHLGVSPLCDRHTESIAXIQIGN 424

Qy        361 MTYL 364
              |||
Db        425 YTYL 428


RESULT 5
US-10-258-746-2
; Sequence 2, Application US/10258746
; Publication No. US20030138815A1
; GENERAL INFORMATION:
;  APPLICANT: Merck Patent GmbH
;  TITLE OF INVENTION: New Phosphodiesterase type 7
;  FILE REFERENCE: PDE7spliceFWKWS
;  CURRENT APPLICATION NUMBER: US/10/258,746
;  CURRENT FILING DATE:  2002-10-28
;  NUMBER OF SEQ ID NOS: 4
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
;    LENGTH: 336
;    TYPE: PRT
;    ORGANISM: Homo sapiens
US-10-258-746-2

  Query Match             79.7%;  Score 1787;  DB 14;  Length 336;
  Best Local Similarity   100.0%;  Pred. No. 9.7e-178;
  Matches  336;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         91 MLEKVGNWNFDIFLFDRLTNGNSLVSLTFHLFSLHGLIEYFHLDMMKLRRFLVMIQEDYH 150
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MLEKVGNWNFDIFLFDRLTNGNSLVSLTFHLFSLHGLIEYFHLDMMKLRRFLVMIQEDYH 60

Qy        151 SQNPYHNAVHAADVTQAMHCYLKEPKLANSVTPWDILLSLIAAATHDLDHPGVNQPFLIK 210
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 SQNPYHNAVHAADVTQAMHCYLKEPKLANSVTPWDILLSLIAAATHDLDHPGVNQPFLIK 120

Qy        211 TNHYLATLYKNTSVLENHHWRSAVGLLRESGLFSHLPLESRQQMETQIGALILATDISRQ 270
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 TNHYLATLYKNTSVLENHHWRSAVGLLRESGLFSHLPLESRQQMETQIGALILATDISRQ 180

Qy        271 NEYLSLFRSHLDRGDLCLEDTRHRHLVLQMALKCADICNPCRTWELSKQWSEKVTEEFFH 330
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 NEYLSLFRSHLDRGDLCLEDTRHRHLVLQMALKCADICNPCRTWELSKQWSEKVTEEFFH 240

Qy        331 QGDIEKKYHLGVSPLCDRHTESIANIQIGFMTYLVEPLFTEWARFSNTRLSQTMLGHVGL 390
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 QGDIEKKYHLGVSPLCDRHTESIANIQIGFMTYLVEPLFTEWARFSNTRLSQTMLGHVGL 300

Qy        391 NKASWKGLQREQSSSEDTDAAFELNSQLLPQENRLS 426
              |||||||||||||||||||||||||||||||||||
Db        301 NKASWKGLQREQSSSEDTDAAFELNSQLLPQENRLS 336


RESULT 6
US-10-311-104-1
; Sequence 1, Application US/10311104
; Publication No. US20040054138A1
; GENERAL INFORMATION:
;  APPLICANT: INCYTE GENOMICS, INC.
;  APPLICANT:  THORNTON, Michael
;  APPLICANT:  DING, Li
;  APPLICANT:  ARIVZU Chandra S.
;  APPLICANT:  YAO, Monique G.
;  APPLICANT:  TRIBOULEY, Catherine M.
;  APPLICANT:  LAL, Preeti G.
;  APPLICANT:  HAFALIA, April J. A.
;  APPLICANT:  BAUGHN, Mariah R.
;  APPLICANT:  RAMKUMAR, Jayalaxmi
;  APPLICANT:  LU, Yan
;  APPLICANT:  Chawla, Narinder K.
;  TITLE OF INVENTION: PHOSPHODIESTERASES
;  FILE REFERENCE: PI-0136 PCT
;  CURRENT APPLICATION NUMBER: US/10/311,104
;  CURRENT FILING DATE:  2002-12-12
;  PRIOR APPLICATION NUMBER: PCT/US01/20140
;  PRIOR FILING DATE: 2001-06-21
;  PRIOR APPLICATION NUMBER: 60/213,741
;  PRIOR FILING DATE: 2000-06-22
;  PRIOR APPLICATION NUMBER: 60/218,234
;  PRIOR FILING DATE: 2000-07-14
;  PRIOR APPLICATION NUMBER: 60/241,100
;  PRIOR FILING DATE: 2000-10-16
;  NUMBER OF SEQ ID NOS: 8
;  SOFTWARE: PERL Program
; SEQ ID NO 1
;    LENGTH: 502
;    TYPE: PRT
;    ORGANISM: Homo sapiens
;    FEATURE:
;    NAME/KEY: misc_feature
;    OTHER INFORMATION: Incyte ID No. US20040054138A1 7476201CD1
US-10-311-104-1

  Query Match             61.7%;  Score 1383.5;  DB 12;  Length 502;
  Best Local Similarity   62.9%;  Pred. No. 2.6e-135;
  Matches  253;  Conservative   65;  Mismatches   83;  Indels    1;  Gaps    1;

Qy         11 GDVRVRSRAGFESERRGSHPYIDFRIFHSQSEIEVSVSARNIRRLLSFQRYLRSSRFFRG 70
              ||:|:| : |  :|||||:|:||||: :| :      : : ::|||||||| :||  ||
Db         80 GDIRLRGQTGVRAERRGSYPFIDFRLLNSTTYSGEIGTKKKVKRLLSFQRYFHASRLLRG 139

Qy         71 TAVSNSLNILDDDYNGQAKCMLEKVGNWNFDIFLFDRLTNGNSLVSLTFHLFSLHGLIEY 130
                 |::||:|| ||| || ||| |:|||||||||||||:|  |||: |||| :
Db        140 IIPQAPLHLLDEDYLGQARHMLSKVGMWDFDIFLFDRLTNGNSLVTLLCHLFNTHGLIHH 199

Qy        131 FHLDMMKLRRFLVMIQEDYHSQNPYHNAVHAADVTQAMHCYLKEPKLANSVTPWDILLSL 190
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                  | |||: | |||||:||||||||||||||||||||||||||||||||: :|| ||:| |
Db        200 FKLDMVTLHRFLVMVQEDYHSQNPYHNAVHAADVTQAMHCYLKEPKLASFLTPLDIMLGL 259

Qy        191 IAAATHDLDHPGVNQPFLIKTNHYLATLYKNTSVLENHHWRSAVGLLRESGLFSHLPLES 250
              :||| ||:|||||||||||||||:|| ||:| |||||||||| :|:|||| | :||| |
Db        260 LAAAAHDVDHPGVNQPFLIKTNHHLANLYQNMSVLENHHWRSTIGMLRESRLLAHLPKEM 319

Qy        251 RQQMETQIGALILATDISRQNEYLSLFRSHLDRGDLCLEDTRHRHLVLQMALKCADICNP 310
              | :| |:|:|||||||:||||:|:  ::||   || ||| : || :||:|||||||||||
Db        320 TQDIEQQLGSLILATDINRQNEFLTRLKAHLHNKDLRLEDAQDRHFMLQIALKCADICNP 379

Qy        311 CRTWELSKQWSEKVTEEFFHQGDIEKKYHLGVSPLCDRHTESIANIQIGFMTYLVEPLFT 370
              || ||:||||||:| |||: ||::|:|: | :||||::  :|| :|||||||:|:|||||
Db        380 CRIWEMSKQWSERVCEEFYRQGELEQKFELEISPLCNQQKDSIPSIQIGFMSYIVEPLFR 439

Qy        371 EWARFS-NTRLSQTMLGHVGLNKASWKGLQREQSSSEDTDAA 411
              ||| |: |: ||: ||||:  ||| || |  |  |  :  :
Db        440 EWAHFTGNSTLSENMLGHLAHNKAQWKSLLPRQHRSRGSSGS 481
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RESULT 7
US-10-273-517-1
; Sequence 1, Application US/10273517
; Publication No. US20030143588A1
; GENERAL INFORMATION:
; APPLICANT: THORNTON, Michael B.; DING, Li
; APPLICANT: ARVIZU, Chandra S.; YAO, Monique G.
; APPLICANT: TRIBOULEY, Catherine M.; LAL, Preeti G.
; APPLICANT: HAFALIA, April J. A.; BAUGHN, Mariah R.
; APPLICANT: RAMKUMAR, Jayalaxmi; LU, Yan
; APPLICANT: CHAWLA, Narinder K.
; TITLE OF INVENTION: PHOSPHODIESTERASES
; FILE REFERENCE: PI-0136 USA
; CURRENT APPLICATION NUMBER: US/10/273,517
; CURRENT FILING DATE: 2002-10-18
; PRIOR APPLICATION NUMBER: 60/241,100
; PRIOR FILING DATE: 2000-10-16
; PRIOR APPLICATION NUMBER: 60/218,234
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US01/20140
; PRIOR FILING DATE: 2001-06-21
; PRIOR APPLICATION NUMBER: 60/213,741
; PRIOR FILING DATE: 2000-06-22
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PERL Program
; SEQ ID NO 1
; LENGTH: 502
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No. US20030143588A1 7476201CD1
US-10-273-517-1

Query Match 61.7%; Score 1383.5; DB 14; Length 502;
Best Local Similarity 62.9%; Pred. No. 2.6e-135;
Matches 253; Conservative 65; Mismatches 83; Indels 1; Gaps 1;

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Qy         11 GDVRVRSRAGFESERRGSHPYIDFRIFHSQSEIEVSVSARNIRRLLSFQRYLRSSRFFRG 70
              ||:|:| : |  :|||||:|:||||: :| :      : : ::||||||||  :||  ||
Db         80 GDIRLRGQTGVRAERRGSYPFIDFRLLNSTTYSGEIGTKKKVKRLLSFQRYFHASRLLRG 139

Qy         71 TAVSNSLNILDDDYNGQAKCMLEKVGNWNFDIFLFDRLTNGNSLVSLTFHLFSLHGLIEY 130
                    |::||:|| |||: || ||| |:||||||||||||||:|  |||: |||| :
Db        140 IIPQAPLHLLDEDYLGQARHMLSKVGMWDFDIFLFDRLTNGNSLVTLLCHLFNTHGLIHH 199

Qy        131 FHLDMMKLRRFLVMIQEDYHSQNPYHNAVHAADVTQAMHCYLKEPKLANSVTPWDILLSL 190
              | |||: | |||||:|||||||||||||||||||||||||||||||: :|| ||:| |
Db        200 FKLDMVTLHRFLVMVQEDYHSQNPYHNAVHAADVTQAMHCYLKEPKLASFLTPLDIMLGL 259

Qy        191 IAAATHDLDHPGVNQPFLIKTNHYLATLYKNTSVLENHHWRSAVGLLRESGLFSHLPLES 250
              :||| ||:|||||||||||||||:|| ||:| |||||||||| :|:|||| | :||| |
Db        260 LAAAAHDVDHPGVNQPFLIKTNHHLANLYQNMSVLENHHWRSTIGMLRESRLLAHLPKEM 319
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Qy        251 RQQMETQIGALILATDISRQNEYLSLFRSHLDRGDLCLEDTRHRHLVLQMALKCADICNP 310
              | :| |:|:|||||||:||||:|:  ::||   || ||| : || :||:|||||||||||
Db        320 TQDIEQQLGSLILATDINRQNEFLTRLKAHLHNKDLRLEDAQDRHFMLQIALKCADICNP 379

Qy        311 CRTWELSKQWSEKVTEEFFHQGDIEKKYHLGVSPLCDRHTESIANIQIGFMTYLVEPLFT 370
              || ||:||||||:| |||: ||::|:|: | :||||::  :|| :|||||||:|:|||||
Db        380 CRIWEMSKQWSERVCEEFYRQGELEQKFELEISPLCNQQKDSIPSIQIGFMSYIVEPLFR 439

Qy        371 EWARFS-NTRLSQTMLGHVGLNKASWKGLQREQSSSEDTDAA 411
              ||| |: |: ||: ||||:  ||| || |  |  |  :  :
Db        440 EWAHFTGNSTLSENMLGHLAHNKAQWKSLLPRQHRSRGSSGS 481
```

RESULT 8
US-10-386-414-4
; Sequence 4, Application US/10386414
; Publication No. US20040006016A1
; GENERAL INFORMATION:
; APPLICANT: Kapeller-Libermann, Rosana
; APPLICANT: Robison, Keith E.
; APPLICANT: White, David
; APPLICANT: Williamson, Mark W.
; APPLICANT: Cook, William James
; APPLICANT: Meyers, Rachel E.
; APPLICANT: MacBeth, Kyle J.
; APPLICANT: Carroll, Joseph M.
; APPLICANT: Chun, Miyoung
; TITLE OF INVENTION: NOVEL 27875, 22025, 27420, 17906, 16319,
; TITLE OF INVENTION: 55092 AND 10218 MOLECULES AND USES THEREFOR
; FILE REFERENCE: MPI03-021OMNIM
; CURRENT APPLICATION NUMBER: US/10/386,414
; CURRENT FILING DATE: 2003-03-11
; PRIOR APPLICATION NUMBER: 09/426,282
; PRIOR FILING DATE: 1999-10-25
; PRIOR APPLICATION NUMBER: 09/668,266
; PRIOR FILING DATE: 2000-09-22
; PRIOR APPLICATION NUMBER: 09/330,970
; PRIOR FILING DATE: 1999-06-11
; PRIOR APPLICATION NUMBER: 09/724,599
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: 09/860,193
; PRIOR FILING DATE: 2001-05-16
; PRIOR APPLICATION NUMBER: 10/283,023
; PRIOR FILING DATE: 2002-10-29
; PRIOR APPLICATION NUMBER: 60/335,044
; PRIOR FILING DATE: 2001-10-31
; PRIOR APPLICATION NUMBER: 10/010,943
; PRIOR FILING DATE: 2001-12-06
; PRIOR APPLICATION NUMBER: 60/254,037
; PRIOR FILING DATE: 2000-12-07
; PRIOR APPLICATION NUMBER: 09/833,082
; PRIOR FILING DATE: 2001-04-10
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 502
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-386-414-4

Query Match 61.7%; Score 1383.5; DB 15; Length 502;
Best Local Similarity 62.9%; Pred. No. 2.6e-135;
Matches 253; Conservative 65; Mismatches 83; Indels 1; Gaps 1;

```
Qy         11 GDVRVRSRAGFESERRGSHPYIDFRIFHSQSEIEVSVSARNIRRLLSFQRYLRSSRFFRG 70
              ||:|:| : |  :|||||:|:||||: :| :      : : ::||||||||  :||  ||
Db         80 GDIRLRGQTGVRAERRGSYPFIDFRLLNSTTYSGEIGTKKKVKRLLSFQRYFHASRLLRG 139

Qy         71 TAVSNSLNILDDDYNGQAKCMLEKVGNWNFDIFLFDRLTNGNSLVSLTFHLFSLHGLIEY 130
                    |::||:|| |||: || ||| |:||||||||||||||:|  |||: |||| :
Db        140 IIPQAPLHLLDEDYLGQARHMLSKVGMWDFDIFLFDRLTNGNSLVTLLCHLFNTHGLIHH 199
```

```
Qy        131 FHLDMMKLRRFLVMIQEDYHSQNPYHNAVHAADVTQAMHCYLKEPKLANSVTPWDILLSL 190
              | |||: | |||||:||||||||||||||||||||||||||||||||||: :|| ||:| |
Db        200 FKLDMVTLHRFLVMVQEDYHSQNPYHNAVHAADVTQAMHCYLKEPKLASFLTPLDIMLGL 259

Qy        191 IAAATHDLDHPGVNQPFLIKTNHYLATLYKNTSVLENHHWRSAVGLLRESGLFSHLPLES 250
              :||| ||:|||||||||||||||:|| ||:| |||||||||| :|:|||| | :||| |
Db        260 LAAAAHDVDHPGVNQPFLIKTNHHLANLYQNMSVLENHHWRSTIGMLRESRLLAHLPKEM 319

Qy        251 RQQMETQIGALILATDISRQNEYLSLFRSHLDRGDLCLEDTRHRHLVLQMALKCADICNP 310
              | :| |:|:|||||||:||||:|:  ::||   || ||| : || :||:||||||||||
Db        320 TQDIEQQLGSLILATDINRQNEFLTRLKAHLHNKDLRLEDAQDRHFMLQIALKCADICNP 379

Qy        311 CRTWELSKQWSEKVTEEFFHQGDIEKKYHLGVSPLCDRHTESIANIQIGFMTYLVEPLFT 370
              || ||:||||||:| |||: ||::|:|: | :||||::  :|| :||||||:|:|||||
Db        380 CRIWEMSKQWSERVCEEFYRQGELEQKFELEISPLCNQQKDSIPSIQIGFMSYIVEPLFR 439

Qy        371 EWARFS-NTRLSQTMLGHVGLNKASWKGLQREQSSSEDTDAA 411
              ||| |: |: ||: |||||:  ||| || |   |  |  :  :
Db        440 EWAHFTGNSTLSENMLGHLAHNKAQWKSLLPRQHRSRGSSGS 481


RESULT 9
US-09-764-898-280
; Sequence 280, Application US/09764898
; Patent No. US20020090673A1
; GENERAL INFORMATION:
;  APPLICANT: Rosen et al.
;  TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
;  FILE REFERENCE: PJZ01
;  CURRENT APPLICATION NUMBER: US/09/764,898
;  CURRENT FILING DATE:  2001-01-17
;  Prior application data removed - consult PALM or file wrapper
;  NUMBER OF SEQ ID NOS: 311
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 280
;   LENGTH: 211
;   TYPE: PRT
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: SITE
;   LOCATION: (198)
;   OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-764-898-280

  Query Match             48.1%;  Score 1079;  DB 9;  Length 211;
  Best Local Similarity   98.1%;  Pred. No. 4.7e-104;
  Matches  202;  Conservative    1;  Mismatches    3;  Indels    0;  Gaps    0;

Qy        159 VHAADVTQAMHCYLKEPKLANSVTPWDILLSLIAAATHDLDHPGVNQPFLIKTNHYLATL 218
              :||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          2 IHAADVTQAMHCYLKEPKLANSVTPWDILLSLIAAATHDLDHPGVNQPFLIKTNHYLATL 61

Qy        219 YKNTSVLENHHWRSAVGLLRESGLFSHLPLESRQQMETQIGALILATDISRQNEYLSLFR 278
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 YKNTSVLENHHWRSAVGLLRESGLFSHLPLESRQQMETQIGALILATDISRQNEYLSLFR 121

Qy        279 SHLDRGDLCLEDTRHRHLVLQMALKCADICNPCRTWELSKQWSEKVTEEFFHQGDIEKKY 338
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        122 SHLDRGDLCLEDTRHRHLVLQMALKCADICNPCRTWELSKQWSEKVTEEFFHQGDIEKKY 181

Qy        339 HLGVSPLCDRHTESIANIQIGFMTYL 364
              |||||||||||||| ||||  |||
Db        182 HLGVSPLCDRHTESIAXIQIGNYTYL 207


RESULT 10
US-09-989-442-120
; Sequence 120, Application US/09989442
; Publication No. US20030013649A1
; GENERAL INFORMATION:
;  APPLICANT: Rosen et al.
;  TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
;  FILE REFERENCE: PJZ08
;  CURRENT APPLICATION NUMBER: US/09/989,442
;  CURRENT FILING DATE:  2001-11-21
;  PRIOR APPLICATION NUMBER: 60/179,065
;  PRIOR FILING DATE: 2000-01-31
;  PRIOR APPLICATION NUMBER: 60/180,628
;  PRIOR FILING DATE: 2000-02-04
;  PRIOR APPLICATION NUMBER: 60/214,886
;  PRIOR FILING DATE: 2000-06-28
;  PRIOR APPLICATION NUMBER: 60/217,487
;  PRIOR FILING DATE: 2000-07-11
;  PRIOR APPLICATION NUMBER: 60/225,758
;  PRIOR FILING DATE: 2000-08-14
;  PRIOR APPLICATION NUMBER: 60/220,963
;  PRIOR FILING DATE: 2000-07-26
;  PRIOR APPLICATION NUMBER: 60/217,496
;  PRIOR FILING DATE: 2000-07-11
;  PRIOR APPLICATION NUMBER: 60/225,447
;  PRIOR FILING DATE: 2000-08-14
;  PRIOR APPLICATION NUMBER: 60/218,290
;  PRIOR FILING DATE: 2000-07-14
;  PRIOR APPLICATION NUMBER: 60/225,757
;  PRIOR FILING DATE: 2000-08-14
;  PRIOR APPLICATION NUMBER: 60/226,868
;  PRIOR FILING DATE: 2000-08-22
;  PRIOR APPLICATION NUMBER: 60/216,647
;  PRIOR FILING DATE: 2000-07-07
;  PRIOR APPLICATION NUMBER: 60/225,267
;  PRIOR FILING DATE: 2000-08-14
;  PRIOR APPLICATION NUMBER: 60/216,880
;  PRIOR FILING DATE: 2000-07-07
;  PRIOR APPLICATION NUMBER: 60/225,270
;  PRIOR FILING DATE: 2000-08-14
;  PRIOR APPLICATION NUMBER: 60/251,869
;  PRIOR FILING DATE: 2000-12-08
;  PRIOR APPLICATION NUMBER: 60/235,834
;  PRIOR FILING DATE: 2000-09-27
;  PRIOR APPLICATION NUMBER: 60/234,274
;  PRIOR FILING DATE: 2000-09-21
;  PRIOR APPLICATION NUMBER: 60/234,223
;  PRIOR FILING DATE: 2000-09-21
;  PRIOR APPLICATION NUMBER: 60/228,924
;  PRIOR FILING DATE: 2000-08-30
;  PRIOR APPLICATION NUMBER: 60/224,518
;  PRIOR FILING DATE: 2000-08-14
;  PRIOR APPLICATION NUMBER: 60/236,369
;  PRIOR FILING DATE: 2000-09-29
;  PRIOR APPLICATION NUMBER: 60/224,519
;  PRIOR FILING DATE: 2000-08-14
;  PRIOR APPLICATION NUMBER: 60/220,964
;  PRIOR FILING DATE: 2000-07-26
;  PRIOR APPLICATION NUMBER: 60/241,809
;  PRIOR FILING DATE: 2000-10-20
;  PRIOR APPLICATION NUMBER: 60/249,299
;  PRIOR FILING DATE: 2000-11-17
;  PRIOR APPLICATION NUMBER: 60/236,327
;  PRIOR FILING DATE: 2000-09-29
;  PRIOR APPLICATION NUMBER: 60/241,785
;  PRIOR FILING DATE: 2000-10-20
;  PRIOR APPLICATION NUMBER: 60/244,617
;  PRIOR FILING DATE: 2000-11-01
;  PRIOR APPLICATION NUMBER: 60/225,268
;  PRIOR FILING DATE: 2000-08-14
;  PRIOR APPLICATION NUMBER: 60/236,368
;  PRIOR FILING DATE: 2000-09-29
;  PRIOR APPLICATION NUMBER: 60/251,856
;  PRIOR FILING DATE: 2000-12-08
;  PRIOR APPLICATION NUMBER: 60/251,868
;  PRIOR FILING DATE: 2000-12-08
;  PRIOR APPLICATION NUMBER: 60/229,344
;  PRIOR FILING DATE: 2000-09-01
;  PRIOR APPLICATION NUMBER: 60/234,997
;  PRIOR FILING DATE: 2000-09-25
;  PRIOR APPLICATION NUMBER: 60/229,343
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; PRIOR FILING DATE: 2000-09-01
; PRIOR APPLICATION NUMBER: 60/229,345
; PRIOR FILING DATE: 2000-09-01
; PRIOR APPLICATION NUMBER: 60/229,287
; PRIOR FILING DATE: 2000-09-01
; PRIOR APPLICATION NUMBER: 60/229,513
; PRIOR FILING DATE: 2000-09-05
; PRIOR APPLICATION NUMBER: 60/231,413
; PRIOR FILING DATE: 2000-09-08
; PRIOR APPLICATION NUMBER: 60/229,509
; PRIOR FILING DATE: 2000-09-05
; PRIOR APPLICATION NUMBER: 60/236,367
; PRIOR FILING DATE: 2000-09-29
; PRIOR APPLICATION NUMBER: 60/237,039
; PRIOR FILING DATE: 2000-10-02
; PRIOR APPLICATION NUMBER: 60/237,038
; PRIOR FILING DATE: 2000-10-02
; PRIOR APPLICATION NUMBER: 60/236,370
; PRIOR FILING DATE: 2000-09-29
; PRIOR APPLICATION NUMBER: 60/236,802
; PRIOR FILING DATE: 2000-10-02
; PRIOR APPLICATION NUMBER: 60/237,037
; PRIOR FILING DATE: 2000-10-02
; PRIOR APPLICATION NUMBER: 60/237,040
; PRIOR FILING DATE: 2000-10-02
; PRIOR APPLICATION NUMBER: 60/240,960
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/239,935
; PRIOR FILING DATE: 2000-10-13
; PRIOR APPLICATION NUMBER: 60/239,937
; PRIOR FILING DATE: 2000-10-13
; PRIOR APPLICATION NUMBER: 60/241,787
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/246,474
; PRIOR FILING DATE: 2000-11-08
; PRIOR APPLICATION NUMBER: 60/246,532
; PRIOR FILING DATE: 2000-11-08
; PRIOR APPLICATION NUMBER: 60/249,216
; PRIOR FILING DATE: 2000-11-17
; PRIOR APPLICATION NUMBER: 60/249,210
; PRIOR FILING DATE: 2000-11-17
; PRIOR APPLICATION NUMBER: 60/226,681
; PRIOR FILING DATE: 2000-08-22
; PRIOR APPLICATION NUMBER: 60/225,759
; PRIOR FILING DATE: 2000-08-14
; PRIOR APPLICATION NUMBER: 60/225,213
; PRIOR FILING DATE: 2000-08-14
; PRIOR APPLICATION NUMBER: 60/227,182
; PRIOR FILING DATE: 2000-08-22
; PRIOR APPLICATION NUMBER: 60/225,214
; PRIOR FILING DATE: 2000-08-14
; PRIOR APPLICATION NUMBER: 60/235,836
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: 60/230,438
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/215,135
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: 60/225,266
; PRIOR FILING DATE: 2000-08-14
; PRIOR APPLICATION NUMBER: 60/249,218
; PRIOR FILING DATE: 2000-11-17
; PRIOR APPLICATION NUMBER: 60/249,208
; PRIOR FILING DATE: 2000-11-17
; PRIOR APPLICATION NUMBER: 60/249,213
; PRIOR FILING DATE: 2000-11-17
; PRIOR APPLICATION NUMBER: 60/249,212
; PRIOR FILING DATE: 2000-11-17
; PRIOR APPLICATION NUMBER: 60/249,207
; PRIOR FILING DATE: 2000-11-17
; PRIOR APPLICATION NUMBER: 60/249,245
; PRIOR FILING DATE: 2000-11-17
; PRIOR APPLICATION NUMBER: 60/249,244
; PRIOR FILING DATE: 2000-11-17
; PRIOR APPLICATION NUMBER: 60/249,217
; PRIOR FILING DATE: 2000-11-17
; PRIOR APPLICATION NUMBER: 60/249,211
; PRIOR FILING DATE: 2000-11-17
; PRIOR APPLICATION NUMBER: 60/249,215
; PRIOR FILING DATE: 2000-11-17
; PRIOR APPLICATION NUMBER: 60/249,264
; PRIOR FILING DATE: 2000-11-17
; PRIOR APPLICATION NUMBER: 60/249,214
; PRIOR FILING DATE: 2000-11-17
; PRIOR APPLICATION NUMBER: 60/249,297
; PRIOR FILING DATE: 2000-11-17
; PRIOR APPLICATION NUMBER: 60/232,400
; PRIOR FILING DATE: 2000-09-14
; PRIOR APPLICATION NUMBER: 60/231,242
; PRIOR FILING DATE: 2000-09-08
; PRIOR APPLICATION NUMBER: 60/232,081
; PRIOR FILING DATE: 2000-09-08
; PRIOR APPLICATION NUMBER: 60/232,080
; PRIOR FILING DATE: 2000-09-08
; PRIOR APPLICATION NUMBER: 60/231,414
; PRIOR FILING DATE: 2000-09-08
; PRIOR APPLICATION NUMBER: 60/231,244
; PRIOR FILING DATE: 2000-09-08
; PRIOR APPLICATION NUMBER: 60/233,064
; PRIOR FILING DATE: 2000-09-14
; PRIOR APPLICATION NUMBER: 60/233,063
; PRIOR FILING DATE: 2000-09-14
; PRIOR APPLICATION NUMBER: 60/232,397
; PRIOR FILING DATE: 2000-09-14
; PRIOR APPLICATION NUMBER: 60/232,399
; PRIOR FILING DATE: 2000-09-14
; PRIOR APPLICATION NUMBER: 60/232,401
; PRIOR FILING DATE: 2000-09-14
; PRIOR APPLICATION NUMBER: 60/241,808
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/241,826
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/241,786
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/241,221
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/246,475
; PRIOR FILING DATE: 2000-11-08
; PRIOR APPLICATION NUMBER: 60/231,243
; PRIOR FILING DATE: 2000-09-08
; PRIOR APPLICATION NUMBER: 60/233,065
; PRIOR FILING DATE: 2000-09-14

Query Match 48.1%; Score 1079; DB 10; Length 211;
Best Local Similarity 98.1%; Pred. No. 4.7e-104;
Matches 202; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

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Qy        159 VHAADVTQAMHCYLKEPKLANSVTPWDILLSLIAAATHDLDHPGVNQPFLIKTNHYLATL 218
              :|||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          2 IHAADVTQAMHCYLKEPKLANSVTPWDILLSLIAAATHDLDHPGVNQPFLIKTNHYLATL 61

Qy        219 YKNTSVLENHHWRSAVGLLRESGLFSHLPLESRQQMETQIGALILATDISRQNEYLSLFR 278
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 YKNTSVLENHHWRSAVGLLRESGLFSHLPLESRQQMETQIGALILATDISRQNEYLSLFR 121

Qy        279 SHLDRGDLCLEDTRHRHLVLQMALKCADICNPCRTWELSKQWSEKVTEEFFHQGDIEKKY 338
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        122 SHLDRGDLCLEDTRHRHLVLQMALKCADICNPCRTWELSKQWSEKVTEEFFHQGDIEKKY 181

Qy        339 HLGVSPLCDRHTESIANIQIGFMTYL 364
              ||||||||||||||| ||||  |||
Db        182 HLGVSPLCDRHTESIAXIQIGNYTYL 207
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RESULT 11
US-10-386-414-6
; Sequence 6, Application US/10386414

; Publication No. US20040006016A1
; GENERAL INFORMATION:
; APPLICANT: Kapeller-Libermann, Rosana
; APPLICANT: Robison, Keith E.
; APPLICANT: White, David
; APPLICANT: Williamson, Mark W.
; APPLICANT: Cook, William James
; APPLICANT: Meyers, Rachel E.
; APPLICANT: MacBeth, Kyle J.
; APPLICANT: Carroll, Joseph M.
; APPLICANT: Chun, Miyoung
; TITLE OF INVENTION: NOVEL 27875, 22025, 27420, 17906, 16319,
; TITLE OF INVENTION: 55092 AND 10218 MOLECULES AND USES THEREFOR
; FILE REFERENCE: MPI03-021OMNIM
; CURRENT APPLICATION NUMBER: US/10/386,414
; CURRENT FILING DATE: 2003-03-11
; PRIOR APPLICATION NUMBER: 09/426,282
; PRIOR FILING DATE: 1999-10-25
; PRIOR APPLICATION NUMBER: 09/668,266
; PRIOR FILING DATE: 2000-09-22
; PRIOR APPLICATION NUMBER: 09/330,970
; PRIOR FILING DATE: 1999-06-11
; PRIOR APPLICATION NUMBER: 09/724,599
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: 09/860,193
; PRIOR FILING DATE: 2001-05-16
; PRIOR APPLICATION NUMBER: 10/283,023
; PRIOR FILING DATE: 2002-10-29
; PRIOR APPLICATION NUMBER: 60/335,044
; PRIOR FILING DATE: 2001-10-31
; PRIOR APPLICATION NUMBER: 10/010,943
; PRIOR FILING DATE: 2001-12-06
; PRIOR APPLICATION NUMBER: 60/254,037
; PRIOR FILING DATE: 2000-12-07
; PRIOR APPLICATION NUMBER: 09/833,082
; PRIOR FILING DATE: 2001-04-10
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 320
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-386-414-6

Query Match 38.8%; Score 871; DB 15; Length 320;
Best Local Similarity 66.9%; Pred. No. 4.7e-82;
Matches 160; Conservative 34; Mismatches 45; Indels 0; Gaps 0;

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Qy          11 GDVRVRSRAGFESERRGSHPYIDFRIFHSQSEIEVSVSARNIRRLLSFQRYLRSSRFFRG 70
               ||:|:| : |  :|||||:|:|||| :| :      : : ::|||||||  :||  ||
Db          80 GDIRLRGQTGVRAERRGSYPFIDFRLLNSTTYSGEIGTKKKVKRLLSFQRYFHASRLLRG 139

Qy          71 TAVSNSLNILDDDYNGQAKCMLEKVGNWNFDIFLFDRLTNGNSLVSLTFHLFSLHGLIEY 130
                     |::||:|| |||: || ||| |:||||||||||||||||:|  |||: |||| :
Db         140 IIPQAPLHLLDEDYLGQARHMLSKVGMWDFDIFLFDRLTNGNSLVTLLCHLFNTHGLIHH 199

Qy         131 FHLDMMKLRRFLVMIQEDYHSQNPYHNAVHAADVTQAMHCYLKEPKLANSVTPWDILLSL 190
               | |||: | |||||:||||||||||||||||||||||||||||||: :|| ||:| |
Db         200 FKLDMVTLHRFLVMVQEDYHSQNPYHNAVHAADVTQAMHCYLKEPKLASFLTPLDIMLGL 259

Qy         191 IAAATHDLDHPGVNQPFLIKTNHYLATLYKNTSVLENHHWRSAVGLLRESGLFSHLPLE 249
               :||| ||:|||||||||||||:|| ||:| |||||||||| :|:|||| | :||| |
Db         260 LAAAAHDVDHPGVNQPFLIKTNHHLANLYQNMSVLENHHWRSTIGMLRESRLLAHLPKE 318
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RESULT 12
US-10-272-970-17
; Sequence 17, Application US/10272970
; Publication No. US20030139578A1
; GENERAL INFORMATION:
; APPLICANT: Au-Young, Janice K.
; APPLICANT: Cocks, Benjamin G.
; APPLICANT: Coleman, Roger T.
; APPLICANT: Seilhamer, Jeffrey J.
; APPLICANT: Fisher, Douglas A.
; TITLE OF INVENTION: ANTIBODIES SPECIFICALLY BINDING PDE8A and PDE8B
; FILE REFERENCE: PC-0054 CIP
; CURRENT APPLICATION NUMBER: US/10/272,970
; CURRENT FILING DATE: 2002-10-15
; PRIOR APPLICATION NUMBER: 09/454,060
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: 09/255,748
; PRIOR FILING DATE: 1999-02-23
; PRIOR APPLICATION NUMBER: 08/974,565
; PRIOR FILING DATE: 1997-11-19
; PRIOR APPLICATION NUMBER: 08/624,663
; PRIOR FILING DATE: 1996-03-25
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PERL Program
; SEQ ID NO 17
; LENGTH: 610
; TYPE: PRT
; ORGANISM: Rattus norvegicus
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: GenBank ID No. US20030139578A1 g1705952
US-10-272-970-17

Query Match 24.7%; Score 555; DB 14; Length 610;
Best Local Similarity 32.6%; Pred. No. 1.3e-48;
Matches 127; Conservative 77; Mismatches 154; Indels 32; Gaps 7;

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Qy           8 RMLGDVRVRSRAGFESERRGSHPYIDFRIFHSQSEIEVSVSARNIRRLLSFQR----YLR 63
               | |  :   ||:| :     |: ::|      |:|:|:       |   :||:     ||
Db          29 RELTHLSEMSRSGNQVSEYISNTFLD-----KQNEVEIPSPTPRQR---AFQQPPPSVLR 80

Qy          64 SSR------FFRGTAVSNSLNI------LDDDYNGQAKCMLEKVGNWNFDIFLFDRLTNG 111
                |:       :    : |||       :  |         || :  |  :||       |
Db          81 QSQPMSQITGLKKLVHTGSLNTNVPRFGVKTDQEDLLAQELENLSKWGLNIFCVSEYAGG 140

Qy         112 NSLVSLTFHLFSLHGLIEYFHLDMMKLRRFLVMIQEDYHSQNPYHNAVHAADVTQAMHCY 171
                ||  : : :|    |:: ||: :  :  ::: ::: ||:   |||::||||| |: |
Db         141 RSLSCIMYTIFQERDLLKKFHIPVDTMMMYMLTLEDHYHADVAYHNSLHAADVLQSTHVL 200

Qy         172 LKEPKLANSVTPWDILLSLIAAATHDLDHPGVNQPFLIKTNHYLATLYKNTSVLENHHWR 231
               |  | |    |  :|| :| ||| ||:|||||:  ||| ||  || :| : |||||||
Db         201 LATPALDAVFTDLEILAALFAAAIHDVDHPGVSNQFLINTNSELALMYNDESVLENHHLA 260

Qy         232 SAVGLLRESG--LFSHLPLESRQQMETQIGALILATDISRQNEYLSLFRSHLD------R 283
                  ||:|    :| :|    || :   :  ::||||:|:    |:  :: ::
Db         261 VGFKLLQEENCDIFQNLSKRQRQSLRKMVIDMVLATDMSKHMTLLADLKTMVETKKVTSS 320

Qy         284 GDLCLEDTRHRHLVLQMALKCADICNPCRTWELSKQWSEKVTEEFFHQGDIEKKYHLGVS 343
               | | |::   |  ||:  : |||: || :  || :||:::  ||| ||| |::  : :|
Db         321 GVLLLDNYSDRIQVLRNMVHCADLSNPTKPLELYRQWTDRIMAEFFQQGDRERERGMEIS 380

Qy         344 PLCDRHTESIANIQIGFMTYLVEPLFTEWA 373
               |:||:|| |:   |:||: |:| ||:  ||
Db         381 PMCDKHTASVEKSQVGFIDYIVHPLWETWA 410
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RESULT 13
US-10-627-929-9
; Sequence 9, Application US/10627929
; Publication No. US20040018605A1
; GENERAL INFORMATION:
; APPLICANT: Au-Young, Janice; Cocks, Benjamin G.
; APPLICANT: Coleman, Roger; Seilhamer, Jeffrey J.
; APPLICANT: Fisher, Douglas A.
; TITLE OF INVENTION: CYCLIC NUCLEOTIDE PHOSPHODIESTERASES
; FILE REFERENCE: PF-0057-4 CON
; CURRENT APPLICATION NUMBER: US/10/627,929
; CURRENT FILING DATE: 2003-07-25
; PRIOR APPLICATION NUMBER: US 09/454,060
; PRIOR FILING DATE: 1999-12-02
; PRIOR APPLICATION NUMBER: US 08/974,565

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;  PRIOR FILING DATE: 1997-11-19
;  NUMBER OF SEQ ID NOS: 18
;  SOFTWARE: PERL Program
; SEQ ID NO 9
;   LENGTH: 610
;   TYPE: PRT
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   OTHER INFORMATION: GenBank ID No. US20040018605A1 g1705952
US-10-627-929-9

  Query Match            24.7%;  Score 555;  DB 15;  Length 610;
  Best Local Similarity  32.6%;  Pred. No. 1.3e-48;
  Matches  127;  Conservative   77;  Mismatches  154;  Indels   32;  Gaps    7;

Qy          8 RMLGDVRVRSRAGFESERRGSHPYIDFRIFHSQSEIEVSVSARNIRRLLSFQR----YLR 63
              | |   :   ||:| :     |: ::|      |:|:|:       |   :||:     ||
Db         29 RELTHLSEMSRSGNQVSEYISNTFLD-----KQNEVEIPSPTPRQR---AFQQPPPSVLR 80

Qy         64 SSR------FFRGTAVSNSLNI------LDDDYNGQAKCMLEKVGNWNFDIFLFDRLTNG 111
               |:      :    : |||       : |       || :  |  :||       |
Db         81 QSQPMSQITGLKKLVHTGSLNTNVPRFGVKTDQEDLLAQELENLSKWGLNIFCVSEYAGG 140

Qy        112 NSLVSLTFHLFSLHGLIEYFHLDMMKLRRFLVMIQEDYHSQNPYHNAVHAADVTQAMHCY 171
              ||   : : :|    |:: ||: :  :  ::: ::: ||:   |||::||||| |: |
Db        141 RSLSCIMYTIFQERDLLKKFHIPVDTMMMYMLTLEDHYHADVAYHNSLHAADVLQSTHVL 200

Qy        172 LKEPKLANSVTPWDILLSLIAAATHDLDHPGVNQPFLIKTNHYLATLYKNTSVLENHHWR 231
              |  | |    | :|| :| ||| ||:|||||:  ||| ||  || :| : |||||||
Db        201 LATPALDAVFTDLEILAALFAAAIHDVDHPGVSNQFLINTNSELALMYNDESVLENHHLA 260

Qy        232 SAVGLLRESG--LFSHLPLESRQQMETQIGALILATDISRQNEYLSLFRSHLD------R 283
                ||:|    :| :|    || :   :  ::||||:|:    |:  :: ::
Db        261 VGFKLLQEENCDIFQNLSKRQRQSLRKMVIDMVLATDMSKHMTLLADLKTMVETKKVTSS 320

Qy        284 GDLCLEDTRHRHLVLQMALKCADICNPCRTWELSKQWSEKVTEEFFHQGDIEKKYHLGVS 343
              | | |::    |  ||:  : |||: || :  || :||:::  ||| ||| |::  : :|
Db        321 GVLLLDNYSDRIQVLRNMVHCADLSNPTKPLELYRQWTDRIMAEFFQQGDRERERGMEIS 380

Qy        344 PLCDRHTESIANIQIGFMTYLVEPLFTEWA 373
              |:||:|| |:   |:||: |:| ||:  ||
Db        381 PMCDKHTASVEKSQVGFIDYIVHPLWETWA 410


RESULT 14
US-09-983-754-2
; Sequence 2, Application US/09983754
; Publication No. US20030064374A1
; GENERAL INFORMATION:
;  APPLICANT: EXONHIT THERAPEUTICS SA
;  APPLICANT:  AIT IKHLEF, ali
;  APPLICANT:  RESINK, Annelies
;  APPLICANT:  SCHWEIGHOFFER, Fabien
;  TITLE OF INVENTION: Molecular Target of Neurotoxicity
;  FILE REFERENCE: B0100US
;  CURRENT APPLICATION NUMBER: US/09/983,754
;  CURRENT FILING DATE:  2001-10-25
;  NUMBER OF SEQ ID NOS: 4
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
;   LENGTH: 721
;   TYPE: PRT
;   ORGANISM: souris
US-09-983-754-2

  Query Match            24.6%;  Score 551;  DB 12;  Length 721;
  Best Local Similarity  31.8%;  Pred. No. 4.3e-48;
  Matches  122;  Conservative   84;  Mismatches  152;  Indels   26;  Gaps    6;

Qy          8 RMLGDVRVRSRAGFESERRGSHPYIDFRIFHSQSEIEVSVSARNIRR---------LLSF 58
              | |   :   ||:| :     |: ::|      |:::|:    :  |          :|
Db        241 RELTHLSEMSRSGNQVSEYISNTFLD-----KQNDVEIPSPTQKDREKKKKQQLMTQISG 295

Qy         59 QRYLRSSRFFRGTAVSN-SLNILDDDYNGQAKCMLEKVGNWNFDIFLFDRLTNGNSLVSL 117
               : |  |     |::|   :|  ::|:  :    || :  |  :||    ::    |  :
Db        296 VKKLMHSSSLNNTSISRFGINTENEDHLAKE---LEDLNKWGLNIFNVAGYSHNRPLTCI 352

Qy        118 TFHLFSLHGLIEYFHLDMMKLRRFLVMIQEDYHSQNPYHNAVHAADVTQAMHCYLKEPKL 177
               : :|     |:: | :        ::: ::: |||   |||::|||| |: |  |  | |
Db        353 MYAIFQERDLLKTFKISSDTFVTYMMTLEDHYHSDVAYHNSLHAADVAQSTHVLLSTPAL 412

Qy        178 ANSVTPWDILLSLIAAATHDLDHPGVNQPFLIKTNHYLATLYKNTSVLENHHWRSAVGLL 237
                  |  :|| :: ||| ||:|||||:  ||| ||  || :| : |||||||       ||
Db        413 DAVFTDLEILAAIFAAAIHDVDHPGVSNQFLINTNSELALMYNDESVLENHHLAVGFKLL 472

Qy        238 RES--GLFSHLPLESRQQMETQIGALILATDISRQNEYLSLFRSHLD------RGDLCLE 289
               :|    :| :|  : || :   :  ::||||:|:    |:  :: ::      | | |:
Db        473 QEEHCDIFQNLTKKQRQTLRKMVIDMVLATDMSKHMSLLADLKTMVETKKVTSSGVLLLD 532

Qy        290 DTRHRHLVLQMALKCADICNPCRTWELSKQWSEKVTEEFFHQGDIEKKYHLGVSPLCDRH 349
               :  | ||:  : |||: || :: || :||:::: |||| ||| |::  : :||:||:|
Db        533 NYTDRIQVLRNMVHCADLSNPTKSLELYRQWTDRIMEEFFQQGDKERERGMEISPMCDKH 592

Qy        350 TESIANIQIGFMTYLVEPLFTEWA 373
              | |:   |:||: |:| ||:  ||
Db        593 TASVEKSQVGFIDYIVHPLWETWA 616


RESULT 15
US-10-442-675-2
; Sequence 2, Application US/10442675
; Publication No. US20040086900A1
; GENERAL INFORMATION:
;  APPLICANT: Wigler, M.
;  APPLICANT:  Colicelli, J.
;  TITLE OF INVENTION: Method for Identifying Modulators Gene Expression
;  FILE REFERENCE: 27866/39366
;  CURRENT APPLICATION NUMBER: US/10/442,675
;  CURRENT FILING DATE:  2003-05-21
;  NUMBER OF SEQ ID NOS: 20
;  SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
;   LENGTH: 517
;   TYPE: PRT
;   ORGANISM: Rattus norvegicus
US-10-442-675-2

  Query Match            24.5%;  Score 550;  DB 16;  Length 517;
  Best Local Similarity  31.8%;  Pred. No. 3.4e-48;
  Matches  122;  Conservative   84;  Mismatches  152;  Indels   26;  Gaps    6;

Qy          8 RMLGDVRVRSRAGFESERRGSHPYIDFRIFHSQSEIEVSVSARNIRR---------LLSF 58
              | |   :   ||:| :     |: ::|      |:::|:    :  |          :|
Db         37 RELTHLSEMSRSGNQVSEYISNTFLD-----KQNDVEIPSPTQKDREKKKKQQLMTQISG 91

Qy         59 QRYLRSSRFFRGTAVSN-SLNILDDDYNGQAKCMLEKVGNWNFDIFLFDRLTNGNSLVSL 117
               : |  |     |::|   :|  ::|:  :    || :  |  :||    ::    |  :
Db         92 VKKLMHSSSLNNTSISRFGVNTENEDHLAKE---LEDLNKWGLNIFNVAGYSHNRPLTCI 148

Qy        118 TFHLFSLHGLIEYFHLDMMKLRRFLVMIQEDYHSQNPYHNAVHAADVTQAMHCYLKEPKL 177
               : :|     |:: | :        ::: ::: |||   |||::|||| |: |  |  | |
Db        149 MYAIFQERDLLKTFKISSDTFVTYMMTLEDHYHSDVAYHNSLHAADVAQSTHVLLSTPAL 208

Qy        178 ANSVTPWDILLSLIAAATHDLDHPGVNQPFLIKTNHYLATLYKNTSVLENHHWRSAVGLL 237
                  |  :|| :: ||| ||:|||||:  ||| ||  || :| : |||||||       ||
Db        209 DAVFTDLEILAAIFAAAIHDVDHPGVSNQFLINTNSELALMYNDESVLENHHLAVGFKLL 268

Qy        238 RES--GLFSHLPLESRQQMETQIGALILATDISRQNEYLSLFRSHLD------RGDLCLE 289
               :|    :| :|  : || :   :  ::||||:|:    |:  :: ::      | | |:
Db        269 QEEHCDIFQNLTKKQRQTLRKMVIDMVLATDMSKHMSLLADLKTMVETKKVTSSGVLLLD 328

Qy        290 DTRHRHLVLQMALKCADICNPCRTWELSKQWSEKVTEEFFHQGDIEKKYHLGVSPLCDRH 349
               :  | ||:  : |||: || :: || :||:::: |||| ||| |::  : :||:||:|
Db        329 NYTDRIQVLRNMVHCADLSNPTKSLELYRQWTDRIMEEFFQQGDKERERGMEISPMCDKH 388
```

```
Qy        350 TESIANIQIGFMTYLVEPLFTEWA 373
              | |:   |:||: |:| ||:  ||
Db        389 TASVEKSQVGFIDYIVHPLWETWA 412
```

Search completed: May 26, 2004, 09:42:42
Job time : 578 secs

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: May 26, 2004, 09:24:28 ; Search time 21 Seconds
(without alignments)
1951.314 Million cell updates/sec

Title: US-09-966-781A-1
Perfect score: 2243
Sequence: 1 DQTALYIRMLGDVRVRSRAG.....DTDAAFELNSQLLPQENRLS 426

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_78:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	2243	100.0	498	2	A47286	3',5'-cyclic-AMP p
2	1403.5	62.6	450	2	JC7266	3',5'-cyclic-nucle
3	555	24.7	610	2	I67946	3',5'-cyclic-nucle
4	555	24.7	844	2	I53865	phosphodiesterase
5	550	24.5	562	2	I59143	cAMP phosphodieste
6	550	24.5	564	2	JC1519	3',5'-cyclic-nucle
7	550	24.5	564	2	A40949	cyclic-AMP phospho
8	550	24.5	736	2	I61354	phosphodiesterase
9	542	24.2	673	2	I61358	3',5'-cyclic-nucle
10	541	24.1	886	2	A54442	3',5'-cyclic-nucle
11	539	24.0	584	2	B53109	3',5'-cyclic-nucle
12	539	24.0	672	2	I61259	3',5'-cyclic-nucle
13	536	23.9	712	2	S71626	3',5'-cyclic-nucle
14	534.5	23.8	536	2	I67945	3',5'-cyclic-nucle
15	503	22.4	713	2	JW0088	3',5'-cyclic-nucle
16	493.5	22.0	549	2	T16769	hypothetical prote
17	489	21.8	323	2	S55348	3',5'-cyclic-nucle
18	482	21.5	664	2	T24459	hypothetical prote
19	478.5	21.3	777	2	S65543	3',5'-cyclic-nucle
20	471.5	21.0	659	2	JE0293	3',5'-cyclic-nucle
21	471.5	21.0	885	2	JC7898	3',5'-cyclic nucle
22	470.5	21.0	534	1	A44162	3',5'-cyclic-nucle
23	470.5	21.0	535	1	A46378	3',5'-cyclic-nucle
24	470	21.0	267	2	B33904	cAMP phosphodieste
25	469.5	20.9	535	1	A44161	3',5'-cyclic-nucle
26	461	20.6	768	2	T10796	3',5'-cyclic-nucle
27	457.5	20.4	536	1	JC6129	3',5'-cyclic-nucle
28	452	20.2	519	2	T14783	hypothetical prote
29	439.5	19.6	530	1	A45334	3',5'-cyclic-nucle
30	409	18.2	1054	2	T30901	cyclic nucleotide
31	402.5	17.9	1112	2	S70522	cyclic nucleotide
32	393.5	17.5	491	2	A40283	3',5'-cyclic-nucle
33	385.5	17.2	1108	2	A48508	cyclic-nucleotide
34	375	16.7	1141	2	A44093	cGMP-inhibited cAM
35	347.5	15.5	875	1	JW0106	3',5'-cyclic-GMP p
36	335	14.9	875	1	A48719	3',5'-cyclic-GMP p
37	327	14.6	921	1	A40981	3',5'-cyclic-nucle
38	323	14.4	928	1	JC2486	3',5'-cyclic-nucle
39	297	13.2	859	2	B34611	3',5'-cyclic-GMP p
40	292	13.0	856	2	S30762	3',5'-cyclic-GMP p
41	290	12.9	859	2	S13030	3',5'-cyclic-GMP p
42	289.5	12.9	859	1	S06418	3',5'-cyclic-GMP p
43	288	12.8	858	2	JC4520	3',5'-cyclic-GMP p
44	287	12.8	856	1	A47451	3',5'-cyclic-GMP p
45	286.5	12.8	854	2	A42828	3',5'-cyclic-GMP p

ALIGNMENTS

RESULT 1
A47286
3',5'-cyclic-AMP phosphodiesterase (EC 3.1.4.-) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 03-May-1994 #sequence_revision 03-May-1994 #text_change 03-Nov-2000
C;Accession: A47286
R;Michaeli, T.; Bloom, T.J.; Martins, T.; Loughney, K.; Ferguson, K.; Riggs, M.; Rodge:
J. Biol. Chem. 268, 12925-12932, 1993
A;Title: Isolation and characterization of a previously undetected human cAMP phosphod:
A;Reference number: A47286; MUID:93286141; PMID:8389765
A;Accession: A47286
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-498 <MIC>
A;Cross-references: GB:L12052; NID:g179892; PID:g179893
C;Superfamily: 3',5'-cyclic-nucleotide phosphodiesterase 1B, calmodulin-dependent; 3',
C;Keywords: phosphoric diester hydrolase
F;227-447/Domain: 3',5'-cyclic-nucleotide phosphodiesterase homology <CNP>

Query Match 100.0%; Score 2243; DB 2; Length 498;
Best Local Similarity 100.0%; Pred. No. 6.2e-177;
Matches 426; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 DQTALYIRMLGDVRVRSRAGFESERRGSHPYIDFRIFHSQSEIEVSVSARNIRRLLSFQR 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         73 DQTALYIRMLGDVRVRSRAGFESERRGSHPYIDFRIFHSQSEIEVSVSARNIRRLLSFQR 132

Qy         61 YLRSSRFFRGTAVSNSLNILDDDYNGQAKCMLEKVGNWNFDIFLFDRLTNGNSLVSLTFH 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        133 YLRSSRFFRGTAVSNSLNILDDDYNGQAKCMLEKVGNWNFDIFLFDRLTNGNSLVSLTFH 192

Qy        121 LFSLHGLIEYFHLDMMKLRRFLVMIQEDYHSQNPYHNAVHAADVTQAMHCYLKEPKLANS 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        193 LFSLHGLIEYFHLDMMKLRRFLVMIQEDYHSQNPYHNAVHAADVTQAMHCYLKEPKLANS 252

Qy        181 VTPWDILLSLIAAATHDLDHPGVNQPFLIKTNHYLATLYKNTSVLENHHWRSAVGLLRES 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        253 VTPWDILLSLIAAATHDLDHPGVNQPFLIKTNHYLATLYKNTSVLENHHWRSAVGLLRES 312

Qy        241 GLFSHLPLESRQQMETQIGALILATDISRQNEYLSLFRSHLDRGDLCLEDTRHRHLVLQM 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        313 GLFSHLPLESRQQMETQIGALILATDISRQNEYLSLFRSHLDRGDLCLEDTRHRHLVLQM 372

Qy        301 ALKCADICNPCRTWELSKQWSEKVTEEFFHQGDIEKKYHLGVSPLCDRHTESIANIQIGF 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        373 ALKCADICNPCRTWELSKQWSEKVTEEFFHQGDIEKKYHLGVSPLCDRHTESIANIQIGF 432

Qy        361 MTYLVEPLFTEWARFSNTRLSQTMLGHVGLNKASWKGLQREQSSSEDTDAAFELNSQLLP 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        433 MTYLVEPLFTEWARFSNTRLSQTMLGHVGLNKASWKGLQREQSSSEDTDAAFELNSQLLP 492

Qy        421 QENRLS 426
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                |||||||
Db        493 QENRLS 498
```

RESULT 2
JC7266
3',5'-cyclic-nucleotide phosphodiesterase (EC 3.1.4.17) 7B - human
N;Alternate names: cAMP-specific phosphodiesterase 7B
C;Species: Homo sapiens (man)
C;Date: 18-Aug-2000 #sequence_revision 18-Aug-2000 #text_change 17-Nov-2000
C;Accession: JC7266
R;Sasaki, T.; Kotera, J.; Yuasa, K.; Omori, K.
Biochem. Biophys. Res. Commun. 271, 575-583, 2000
A;Title: Identification of human PDE7B, a cAMP-specific phosphodiesterase.
A;Reference number: JC7266
A;Accession: JC7266
A;Molecule type: mRNA
A;Residues: 1-450 <SAS>
A;Cross-references: DDBJ:AB038040
A;Experimental source: caudate nucleus
C;Genetics:
A;Gene: pde7B
A;Map position: 6q23-24
C;Superfamily: 3',5'-cyclic-nucleotide phosphodiesterase 1B, calmodulin-dependent; 3',5'
C;Keywords: phosphoric diester hydrolase

  Query Match 62.6%; Score 1403.5; DB 2; Length 450;
  Best Local Similarity 62.6%; Pred. No. 8.3e-108;
  Matches 258; Conservative 66; Mismatches 87; Indels 1; Gaps 1;

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Qy          1 DQTALYIRMLGDVRVRSRAGFESERRGSHPYIDFRIFHSQSEIEVSVSARNIRRLLSFQR 60
              ||  :  :|||:|:|  : |  :|||||:|:||||: :| :      : : ::|||||||
Db         18 DQNAKCVCMLGDIRLRGQTGVRAERRGSYPFIDFRLLNSTTYSGEIGTKKKVKRLLSFQR 77

Qy         61 YLRSSRFFRGTAVSNSLNILDDDYNGQAKCMLEKVGNWNFDIFLFDRLTNGNSLVSLTFH 120
              |  :||  ||       |::||:|| |||: || ||| |:||||||||||||||:|  |
Db         78 YFHASRLLRGIIPQAPLHLLDEDYLGQARHMLSKVGMWDFDIFLFDRLTNGNSLVTLLCH 137

Qy        121 LFSLHGLIEYFHLDMMKLRRFLVMIQEDYHSQNPYHNAVHAADVTQAMHCYLKEPKLANS 180
              ||: |||| :| |||: | |||||:||||||||||||||||||||||||||||||||:
Db        138 LFNTHGLIHHFKLDMVTLHRFLVMVQEDYHSQNPYHNAVHAADVTQAMHCYLKEPKLASF 197

Qy        181 VTPWDILLSLIAAATHDLDHPGVNQPFLIKTNHYLATLYKNTSVLENHHWRSAVGLLRES 240
              :|| ||:| |:||| ||:||||||||||||||:|| ||:| |||||||||| :|:|||
Db        198 LTPLDIMLGLLAAAAHDVDHPGVNQPFLIKTNHHLANLYQNMSVLENHHWRSTIGMLRES 257

Qy        241 GLFSHLPLESRQQMETQIGALILATDISRQNEYLSLFRSHLDRGDLCLEDTRHRHLVLQM 300
              | :||| |  | :| |:|:|||||||:|||:|:  ::||   || ||| : || :||:
Db        258 RLLAHLPKEMTQDIEQQLGSLILATDINRQNEFLTRLKAHLHNKDLRLEDAQDRHFMLQI 317

Qy        301 ALKCADICNPCRTWELSKQWSEKVTEEFFHQGDIEKKYHLGVSPLCDRHTESIANIQIGF 360
              |||||||||||| ||:|||||:| ||| :|::|:|: | :||||::  :|| :|||||
Db        318 ALKCADICNPCRIWEMSKQWSERVCEEFYRQGELEQKFELEISPLCNQQKDSIPSIQIGF 377

Qy        361 MTYLVEPLFTEWARFS-NTRLSQTMLGHVGLNKASWKGLQREQSSSEDTDAA 411
              |:|:||||| ||| |: |: ||: |||||:  ||| || |   |  :  :
Db        378 MSYIVEPLFREWAHFTGNSTLSENMLGHLAHNKAQWKSLLPRQHRSRGSSGS 429
```

RESULT 3
I67946
3',5'-cyclic-nucleotide phosphodiesterase (EC 3.1.4.17) 4A, splice form 1 - rat
N;Alternate names: cyclic AMP-specific phosphodiesterase RD1; RNPDE4A1
N;Contains: 3',5'-cyclic-nucleotide phosphodiesterase 4A, splice form 2 (cyclic AMP-spec
hosphodiesterase RD3)
C;Species: Rattus norvegicus (Norway rat)
C;Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 24-Aug-2001
C;Accession: I67946; A32558; B32558; C32558
R;Bolger, G.B.; Rodgers, L.K.; Riggs, M.
Gene 149, 237-244, 1994
A;Title: Differential CNS expression of alternative mRNA isoforms of the mammalian genes
A;Reference number: I53865; MUID:95047482; PMID:7958996
A;Accession: I67946
A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-610 <RES>
A;Cross-references: GB:L27062; NID:g436013; PIDN:AAA56859.1; PID:g436014
R;Davis, R.L.; Takayasu, H.; Eberwine, M.; Myres, J.
Proc. Natl. Acad. Sci. U.S.A. 86, 3604-3608, 1989
A;Title: Cloning and characterization of mammalian homologs of the Drosophila dunce(+)
A;Reference number: A32558; MUID:89264472; PMID:2542942
A;Accession: A32558
A;Molecule type: mRNA
A;Residues: 1-598,'T',600-610 <DAV>
A;Cross-references: GB:M26715; NID:g203982; PIDN:AAC37699.1; PID:g203983; GB:J04554
A;Accession: B32558
A;Molecule type: mRNA
A;Residues: 85-120,154-598,'T',600-610 <DA2>
A;Cross-references: GB:M26716; GB:M26717; GB:J04554; NID:g203986; PIDN:AAA41102.1; PID
A;Note: splice form RD2
A;Accession: C32558
A;Molecule type: mRNA
A;Residues: 26-598,'T',600-610 <DA3>
A;Cross-references: GB:M26716; NID:g203984; PIDN:AAA41101.1; PID:g203985; GB:J04554
A;Note: splice form RD3
C;Superfamily: 3',5'-cyclic-nucleotide phosphodiesterase 1B, calmodulin-dependent; 3',
C;Keywords: alternative splicing; cAMP binding; phosphoric diester hydrolase
F;14-20/Region: responsible for membrane association
F;26-610/Product: 3',5'-cyclic-nucleotide phosphodiesterase 4A, splice form 3 #status
F;85-120,154-610/Product: 3',5'-cyclic-nucleotide phosphodiesterase 4A, splice form 2
F;184-412/Domain: 3',5'-cyclic-nucleotide phosphodiesterase homology <CNP>

  Query Match 24.7%; Score 555; DB 2; Length 610;
  Best Local Similarity 32.6%; Pred. No. 1.1e-37;
  Matches 127; Conservative 77; Mismatches 154; Indels 32; Gaps 7;

```
Qy          8 RMLGDVRVRSRAGFESERRGSHPYIDFRIFHSQSEIEVSVSARNIRRLLSFQR----YLR 63
              | |  :   ||:| :     |: ::|     |:|:|:       |  :||:    ||
Db         29 RELTHLSEMSRSGNQVSEYISNTFLD-----KQNEVEIPSPTPRQR---AFQQPPPSVLR 80

Qy         64 SSR------FFRGTAVSNSLNI------LDDDYNGQAKCMLEKVGNWNFDIFLFDRLTNG 111
              |:      :   : |||      : |       || : |  :||      |
Db         81 QSQPMSQITGLKKLVHTGSLNTNVPRFGVKTDQEDLLAQELENLSKWGLNIFCVSEYAGG 140

Qy        112 NSLVSLTFHLFSLHGLIEYFHLDMMKLRRFLVMIQEDYHSQNPYHNAVHAADVTQAMHCY 171
              ||  : : :|    |:: ||: :  :  ::: ::: ||:   |||::||||| |: |
Db        141 RSLSCIMYTIFQERDLLKKFHIPVDTMMMYMLTLEDHYHADVAYHNSLHAADVLQSTHVL 200

Qy        172 LKEPKLANSVTPWDILLSLIAAATHDLDHPGVNQPFLIKTNHYLATLYKNTSVLENHHWR 231
              |  | |     |  :|| :| ||| ||:|||||:  ||| ||  || :| : |||||||
Db        201 LATPALDAVFTDLEILAALFAAAIHDVDHPGVSNQFLINTNSELALMYNDESVLENHHLA 260

Qy        232 SAVGLLRESG--LFSHLPLESRQQMETQIGALILATDISRQNEYLSLFRSHLD------R 283
              ||:|    :| :|    || :   :  ::||||:|:    |:  :: ::
Db        261 VGFKLLQEENCDIFQNLSKRQRQSLRKMVIDMVLATDMSKHMTLLADLKTMVETKKVTSS 320

Qy        284 GDLCLEDTRHRHLVLQMALKCADICNPCRTWELSKQWSEKVTEEFFHQGDIEKKYHLGVS 343
              | | |::   |  ||:  : |||: || :  || :||:::  ||| ||| |::  : :|
Db        321 GVLLLDNYSDRIQVLRNMVHCADLSNPTKPLELYRQWTDRIMAEFFQQGDRERERGMEIS 380

Qy        344 PLCDRHTESIANIQIGFMTYLVEPLFTEWA 373
              |:||:|| |:   |:||: |:| ||:  ||
Db        381 PMCDKHTASVEKSQVGFIDYIVHPLWETWA 410
```

RESULT 4
I53865
phosphodiesterase - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 02-Sep-2000
C;Accession: I53865
R;Bolger, G.B.; Rodgers, L.K.; Riggs, M.
Gene 149, 237-244, 1994
A;Title: Differential CNS expression of alternative mRNA isoforms of the mammalian gen
A;Reference number: I53865; MUID:95047482; PMID:7958996
A;Accession: I53865

A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-844 <RES>
A;Cross-references: GB:L27057; NID:g3334904; PIDN:AAC27098.1; PID:g436004
C;Superfamily: 3',5'-cyclic-nucleotide phosphodiesterase homology
F;418-646/Domain: 3',5'-cyclic-nucleotide phosphodiesterase homology <CNP>

Query Match 24.7%; Score 555; DB 2; Length 844;
Best Local Similarity 32.6%; Pred. No. 1.7e-37;
Matches 127; Conservative 77; Mismatches 154; Indels 32; Gaps 7;

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Qy          8 RMLGDVRVRSRAGFESERRGSHPYIDFRIFHSQSEIEVSVSARNIRRLLSFQR----YLR 63
              |  |   :   ||:| :     |: ::|      |:|:|:       |   :||:     ||
Db        263 RELTHLSEMSRSGNQVSEYISNTFLD-----KQNEVEIPSPTPRQR---AFQQPPPSVLR 314

Qy         64 SSR------FFRGTAVSNSLNI------LDDDYNGQAKCMLEKVGNWNFDIFLFDRLTNG 111
               |:      :    : |||       :  |        || :  |  :||       |
Db        315 QSQPMSQITGLKKLVHTGSLNTNVPRFGVKTDQEDLLAQELENLSKWGLNIFCVSEYAGG 374

Qy        112 NSLVSLTFHLFSLHGLIEYFHLDMMKLRRFLVMIQEDYHSQNPYHNAVHAADVTQAMHCY 171
              ||  : : :|    |:: ||: :  :  ::: ::: ||:   |||::||||| |: |
Db        375 RSLSCIMYTIFQERDLLKKFHIPVDTMMMYMLTLEDHYHADVAYHNSLHAADVLQSTHVL 434

Qy        172 LKEPKLANSVTPWDILLSLIAAATHDLDHPGVNQPFLIKTNHYLATLYKNTSVLENHHWR 231
              |  | |    |  :|| :| ||| ||:|||||:  ||| ||  || :| : |||||||
Db        435 LATPALDAVFTDLEILAALFAAAIHDVDHPGVSNQFLINTNSELALMYNDESVLENHHLA 494

Qy        232 SAVGLLRESG--LFSHLPLESRQQMETQIGALILATDISRQNEYLSLFRSHLD------R 283
                ||:|    :| :|    || :   :  ::||||:|:    |:  :: ::
Db        495 VGFKLLQEENCDIFQNLSKRQRQSLRKMVIDMVLATDMSKHMTLLADLKTMVETKKVTSS 554

Qy        284 GDLCLEDTRHRHLVLQMALKCADICNPCRTWELSKQWSEKVTEEFFHQGDIEKKYHLGVS 343
              | | |::   |  ||:  : |||: || :  || :||::::  ||| ||| |::  : :|
Db        555 GVLLLDNYSDRIQVLRNMVHCADLSNPTKPLELYRQWTDRIMAEFFQQGDRERERGMEIS 614

Qy        344 PLCDRHTESIANIQIGFMTYLVEPLFTEWA 373
              |:||:|| |:   |:||: |:| ||:  ||
Db        615 PMCDKHTASVEKSQVGFIDYIVHPLWETWA 644
```

RESULT 5
I59143
cAMP phosphodiesterase - rat (fragment)
C;Species: Rattus norvegicus (Norway rat)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 03-Nov-2000
C;Accession: I59143
R;Colicelli, J.; Birchmeier, C.; Michaeli, T.; O'Neill, K.; Riggs, M.; Wigler, M.
Proc. Natl. Acad. Sci. U.S.A. 86, 3599-3603, 1989
A;Title: Isolation and characterization of a mammalian gene encoding a high-affinity cAM
A;Reference number: I59143; MUID:89264471; PMID:2542941
A;Accession: I59143
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-562 <RES>
A;Cross-references: GB:J04563; NID:g203967; PIDN:AAA66039.1; PID:g203968
C;Superfamily: 3',5'-cyclic-nucleotide phosphodiesterase 1B, calmodulin-dependent; 3',5'
F;231-459/Domain: 3',5'-cyclic-nucleotide phosphodiesterase homology <CNP>

Query Match 24.5%; Score 550; DB 2; Length 562;
Best Local Similarity 31.8%; Pred. No. 2.5e-37;
Matches 122; Conservative 84; Mismatches 152; Indels 26; Gaps 6;

```
Qy          8 RMLGDVRVRSRAGFESERRGSHPYIDFRIFHSQSEIEVSVSARNIRR---------LLSF 58
              |  |   :   ||:| :     |: ::|      |:::|:    :  |          :|
Db         82 RELTHLSEMSRSGNQVSEYISNTFLD-----KQNDVEIPSPTQKDREKKKKQQLMTQISG 136

Qy         59 QRYLRSSRFFRGTAVSN-SLNILDDDYNGQAKCMLEKVGNWNFDIFLFDRLTNGNSLVSL 117
               :  |    |::|   :|  ::|:  :    || :  |  :||     ::   |  :
Db        137 VKKLMHSSSLNNTSISRFGVNTENEDHLAKE---LEDLNKWGLNIFNVAGYSHNRPLTCI 193

Qy        118 TFHLFSLHGLIEYFHLDMMKLRRFLVMIQEDYHSQNPYHNAVHAADVTQAMHCYLKEPKL 177
               : :|    |:: | :      ::: ::: |||   |||::|||| |: |  |  | |
Db        194 MYAIFQERDLLKTFKISSDTFVTYMMTLEDHYHSDVAYHNSLHAADVAQSTHVLLSTPAL 253

Qy        178 ANSVTPWDILLSLIAAATHDLDHPGVNQPFLIKTNHYLATLYKNTSVLENHHWRSAVGLL 237
                  |  :|| :: ||| ||:|||||:  ||| ||  || :| : |||||||      ||
Db        254 DAVFTDLEILAAIFAAAIHDVDHPGVSNQFLINTNSELALMYNDESVLENHHLAVGFKLL 313

Qy        238 RES--GLFSHLPLESRQQMETQIGALILATDISRQNEYLSLFRSHLD------RGDLCLE 289
              :|    :| :|  : || :   :  ::||||:|:    |:  :: ::       | | |:
Db        314 QEEHCDIFQNLTKKQRQTLRKMVIDMVLATDMSKHMSLLADLKTMVETKKVTSSGVLLLD 373

Qy        290 DTRHRHLVLQMALKCADICNPCRTWELSKQWSEKVTEEFFHQGDIEKKYHLGVSPLCDRH 349
              :   |  ||:  : |||: || :: || :||:::: |||| ||| |::  : :||:||:|
Db        374 NYTDRIQVLRNMVHCADLSNPTKSLELYRQWTDRIMEEFFQQGDKERERGMEISPMCDKH 433

Qy        350 TESIANIQIGFMTYLVEPLFTEWA 373
              | |:   |:||: |:| ||:  ||
Db        434 TASVEKSQVGFIDYIVHPLWETWA 457
```

RESULT 6
JC1519
3',5'-cyclic-nucleotide phosphodiesterase (EC 3.1.4.17), cAMP-specific (clone HBP106) -
C;Species: Homo sapiens (man)
C;Date: 14-Jul-1994 #sequence_revision 14-Jul-1994 #text_change 21-Jul-2000
C;Accession: JC1519; A45500; I61359
R;Obernolte, R.; Bhakta, S.; Alvarez, R.; Bach, C.; Zuppan, P.; Mulkins, M.; Jarnagin,
Gene 129, 239-247, 1993
A;Title: The cDNA of a human lymphocyte cyclic-AMP phosphodiesterase (PDE IV) reveals a
A;Reference number: JC1519; MUID:93314968; PMID:8392015
A;Accession: JC1519
A;Molecule type: mRNA
A;Residues: 1-564 <OBE>
A;Cross-references: GB:L12686
A;Experimental source: lymphocyte
A;Note: only partial nucleotide sequence is given
R;McLaughlin, M.M.; Cieslinski, L.B.; Burman, M.; Torphy, T.J.; Livi, G.P.
J. Biol. Chem. 268, 6470-6476, 1993
A;Title: A low-Km, rolipram-sensitive, cAMP-specific phosphodiesterase from human brair
f mRNA.
A;Reference number: A45500; MUID:93203241; PMID:8384210
A;Accession: A45500
A;Molecule type: mRNA
A;Residues: 1-564 <MCL>
A;Cross-references: GB:M97515; NID:g292387; PIDN:AAA36426.1; PID:g292388
A;Experimental source: frontal cortex
A;Note: sequence extracted from NCBI backbone (NCBIN:127929, NCBIP:127930)
R;Bolger, G.; Michaeli, T.; Martins, T.; St. John, T.; Steiner, B.; Rodgers, L.; Riggs,
Mol. Cell. Biol. 13, 6558-6571, 1993
A;Title: A family of human phosphodiesterases homologous to the dunce learning and memc
A;Reference number: A54442; MUID:94019330; PMID:8413254
A;Accession: I61359
A;Status: preliminary; nucleic acid sequence not shown; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-564 <RES>
A;Cross-references: GB:L20971; NID:g347131; PIDN:AAA03593.1; PID:g347132
C;Superfamily: 3',5'-cyclic-nucleotide phosphodiesterase 1B, calmodulin-dependent; 3',5
C;Keywords: phosphoric diester hydrolase
F;233-461/Domain: 3',5'-cyclic-nucleotide phosphodiesterase homology <CNP>

Query Match 24.5%; Score 550; DB 2; Length 564;
Best Local Similarity 31.8%; Pred. No. 2.5e-37;
Matches 122; Conservative 84; Mismatches 152; Indels 26; Gaps 6;

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Qy          8 RMLGDVRVRSRAGFESERRGSHPYIDFRIFHSQSEIEVSVSARNIRR---------LLSF 58
              |  |   :   ||:| :     |: ::|      |:::|:    :  |          :|
Db         84 RELTHLSEMSRSGNQVSEYISNTFLD-----KQNDVEIPSPTQKDREKKKKQQLMTQISG 138

Qy         59 QRYLRSSRFFRGTAVSN-SLNILDDDYNGQAKCMLEKVGNWNFDIFLFDRLTNGNSLVSL 117
               :  |    |::|   :|  ::|:  :    || :  |  :||     ::   |  :
Db        139 VKKLMHSSSLNNTSISRFGVNTENEDHLAKE---LEDLNKWGLNIFNVAGYSHNRPLTCI 195

Qy        118 TFHLFSLHGLIEYFHLDMMKLRRFLVMIQEDYHSQNPYHNAVHAADVTQAMHCYLKEPKL 177
               : :|    |:: | :      ::: ::: |||   |||::|||| |: |  |  | |
Db        196 MYAIFQERDLLKTFRISSDTFITYMMTLEDHYHSDVAYHNSLHAADVAQSTHVLLSTPAL 255
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Qy        178 ANSVTPWDILLSLIAAATHDLDHPGVNQPFLIKTNHYLATLYKNTSVLENHHWRSAVGLL 237
              |  :|| :: ||| ||:|||||:  ||| ||  || :| : |||||||      ||
Db        256 DAVFTDLEILAAIFAAAIHDVDHPGVSNQFLINTNSELALMYNDESVLENHHLAVGFKLL 315

Qy        238 RES--GLFSHLPLESRQQMETQIGALILATDISRQNEYLSLFRSHLD------RGDLCLE 289
              :|    :| :|  : || :   :  ::||||:|:    |:  :: ::       | | |:
Db        316 QEEHCDIFMNLTKKQRQTLRKMVIDMVLATDMSKHMSLLADLKTMVETKKVTSSGVLLLD 375

Qy        290 DTRHRHLVLQMALKCADICNPCRTWELSKQWSEKVTEEFFHQGDIEKKYHLGVSPLCDRH 349
              :  |  ||:  : |||: || :: || :||:::: |||| ||| |::  : :||:||:|
Db        376 NYTDRIQVLRNMVHCADLSNPTKSLELYRQWTDRIMEEFFQQGDKERERGMEISPMCDKH 435

Qy        350 TESIANIQIGFMTYLVEPLFTEWA 373
              | |:   |:||: |:| ||:  ||
Db        436 TASVEKSQVGFIDYIVHPLWETWA 459


RESULT 7
A40949
cyclic-AMP phosphodiesterase (EC 3.1.4.-) - rat
N;Alternate names: PDE4/IVb long form
C;Species: Rattus norvegicus (Norway rat)
C;Date: 13-May-1992 #sequence_revision 13-May-1992 #text_change 09-Jun-2000
C;Accession: A40949; D33904; A53109; I67942
R;Swinnen, J.V.; Tsikalas, K.E.; Conti, M.
J. Biol. Chem. 266, 18370-18377, 1991
A;Title: Properties and hormonal regulation of two structurally related cAMP phosphodies
A;Reference number: A40949; MUID:92011578; PMID:1655746
A;Accession: A40949
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-564 <SWI>
A;Cross-references: GB:M25350
R;Swinnen, J.V.; Joseph, D.R.; Conti, M.
Proc. Natl. Acad. Sci. U.S.A. 86, 5325-5329, 1989
A;Title: Molecular cloning of rat homologues of the Drosophila melanogaster dunce cAMP p
A;Reference number: A33904; MUID:89315790; PMID:2546153
A;Accession: D33904
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 210-476 <SW2>
A;Cross-references: GB:M25350
R;Monaco, L.; Vicini, E.; Conti, M.
J. Biol. Chem. 269, 347-357, 1994
A;Title: Structure of two rat genes coding for closely related rolipram-sensitive cAMP p
A;Reference number: A53109; MUID:94103234; PMID:8276818
A;Accession: A53109
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-358,'S',360-564 <MON>
A;Cross-references: GB:U01291; NID:g409826; PIDN:AAA18926.1; PID:g409828
R;Bolger, G.B.; Rodgers, L.K.; Riggs, M.
Gene 149, 237-244, 1994
A;Title: Differential CNS expression of alternative mRNA isoforms of the mammalian genes
A;Reference number: I53865; MUID:95047482; PMID:7958996
A;Accession: I67942
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-564 <RES>
A;Cross-references: GB:L27058; NID:g950096; PIDN:AAA74478.1; PID:g598375
C;Superfamily: 3',5'-cyclic-nucleotide phosphodiesterase 1B, calmodulin-dependent; 3',5'
C;Keywords: alternative initiators; alternative splicing; phosphoric diester hydrolase
F;233-461/Domain: 3',5'-cyclic-nucleotide phosphodiesterase homology <CNP>

  Query Match             24.5%;  Score 550;  DB 2;  Length 564;
  Best Local Similarity   31.8%;  Pred. No. 2.5e-37;
  Matches  122;  Conservative   84;  Mismatches  152;  Indels   26;  Gaps    6;

Qy          8 RMLGDVRVRSRAGFESERRGSHPYIDFRIFHSQSEIEVSVSARNIRR---------LLSF 58
              | |  :   ||:| :     |: ::|      |:::|:    :  |           :|
Db         84 RELTHLSEMSRSGNQVSEYISNTFLD-----KQNDVEIPSPTQKDREKKKKQQLMTQISG 138

Qy         59 QRYLRSSRFFRGTAVSN-SLNILDDDYNGQAKCMLEKVGNWNFDIFLFDRLTNGNSLVSL 117
               : |  |      |::|   :|  ::|: :    || :  |  :||      ::    | :
Db        139 VKKLMHSSSLNNTSISRFGVNTENEDHLAKE---LEDLNKWGLNIFNVAGYSHNRPLTCI 195

Qy        118 TFHLFSLHGLIEYFHLDMMKLRRFLVMIQEDYHSQNPYHNAVHAADVTQAMHCYLKEPKL 177
               : :|     |:: | :        ::: ::: |||    |||::||||| |: |  |  | |
Db        196 MYAIFQERDLLKTFKISSDTFVTYMMTLEDHYHSDVAYHNSLHAADVAQSTHVLLSTPAL 255

Qy        178 ANSVTPWDILLSLIAAATHDLDHPGVNQPFLIKTNHYLATLYKNTSVLENHHWRSAVGLL 237
              |  :|| :: ||| ||:|||||:  ||| ||  || :| : |||||||      ||
Db        256 DAVFTDLEILAAIFAAAIHDVDHPGVSNQFLINTNSELALMYNDESVLENHHLAVGFKLL 315

Qy        238 RES--GLFSHLPLESRQQMETQIGALILATDISRQNEYLSLFRSHLD------RGDLCLE 289
              :|    :| :|  : || :   :  ::||||:|:    |:  :: ::       | | |:
Db        316 QEEHCDIFQNLTKKQRQTLRKMVIDMVLATDMSKHMSLLADLKTMVETKKVTSSGVLLLD 375

Qy        290 DTRHRHLVLQMALKCADICNPCRTWELSKQWSEKVTEEFFHQGDIEKKYHLGVSPLCDRH 349
              :  |  ||:  : |||: || :: || :||:::: |||| ||| |::  : :||:||:|
Db        376 NYTDRIQVLRNMVHCADLSNPTKSLELYRQWTDRIMEEFFQQGDKERERGMEISPMCDKH 435

Qy        350 TESIANIQIGFMTYLVEPLFTEWA 373
              | |:   |:||: |:| ||:  ||
Db        436 TASVEKSQVGFIDYIVHPLWETWA 459


RESULT 8
I61354
phosphodiesterase - human
C;Species: Homo sapiens (man)
C;Date: 06-Sep-1996 #sequence_revision 06-Sep-1996 #text_change 17-Nov-2000
C;Accession: I61354
R;Bolger, G.; Michaeli, T.; Martins, T.; St. John, T.; Steiner, B.; Rodgers, L.; Riggs,
Mol. Cell. Biol. 13, 6558-6571, 1993
A;Title: A family of human phosphodiesterases homologous to the dunce learning and mem
A;Reference number: A54442; MUID:94019330; PMID:8413254
A;Accession: I61354
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-736 <RES>
A;Cross-references: GB:L20966; NID:g347121; PIDN:AAA03589.1; PID:g347122
C;Superfamily: 3',5'-cyclic-nucleotide phosphodiesterase 1B, calmodulin-dependent; 3',
F;405-633/Domain: 3',5'-cyclic-nucleotide phosphodiesterase homology <CNP>

  Query Match             24.5%;  Score 550;  DB 2;  Length 736;
  Best Local Similarity   31.8%;  Pred. No. 3.7e-37;
  Matches  122;  Conservative   84;  Mismatches  152;  Indels   26;  Gaps    6;

Qy          8 RMLGDVRVRSRAGFESERRGSHPYIDFRIFHSQSEIEVSVSARNIRR---------LLSF 58
              | |  :   ||:| :     |: ::|      |:::|:    :  |           :|
Db        256 RELTHLSEMSRSGNQVSEYISNTFLD-----KQNDVEIPSPTQKDREKKKKQQLMTQISG 310

Qy         59 QRYLRSSRFFRGTAVSN-SLNILDDDYNGQAKCMLEKVGNWNFDIFLFDRLTNGNSLVSL 117
               : |  |      |::|   :|  ::|: :    || :  |  :||      ::    | :
Db        311 VKKLMHSSSLNNTSISRFGVNTENEDHLAKE---LEDLNKWGLNIFNVAGYSHNRPLTCI 367

Qy        118 TFHLFSLHGLIEYFHLDMMKLRRFLVMIQEDYHSQNPYHNAVHAADVTQAMHCYLKEPKL 177
               : :|     |:: | :        ::: ::: |||    |||::||||| |: |  |  | |
Db        368 MYAIFQERDLLKTFRISSDTFITYMMTLEDHYHSDVAYHNSLHAADVAQSTHVLLSTPAL 427

Qy        178 ANSVTPWDILLSLIAAATHDLDHPGVNQPFLIKTNHYLATLYKNTSVLENHHWRSAVGLL 237
              |  :|| :: ||| ||:|||||:  ||| ||  || :| : |||||||      ||
Db        428 DAVFTDLEILAAIFAAAIHDVDHPGVSNQFLINTNSELALMYNDESVLENHHLAVGFKLL 487

Qy        238 RES--GLFSHLPLESRQQMETQIGALILATDISRQNEYLSLFRSHLD------RGDLCLE 289
              :|    :| :|  : || :   :  ::||||:|:    |:  :: ::       | | |:
Db        488 QEEHCDIFMNLTKKQRQTLRKMVIDMVLATDMSKHMSLLADLKTMVETKKVTSSGVLLLD 547

Qy        290 DTRHRHLVLQMALKCADICNPCRTWELSKQWSEKVTEEFFHQGDIEKKYHLGVSPLCDRH 349
              :  |  ||:  : |||: || :: || :||:::: |||| ||| |::  : :||:||:|
Db        548 NYTDRIQVLRNMVHCADLSNPTKSLELYRQWTDRIMEEFFQQGDKERERGMEISPMCDKH 607

Qy        350 TESIANIQIGFMTYLVEPLFTEWA 373
              | |:   |:||: |:| ||:  ||
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Db        608 TASVEKSQVGFIDYIVHPLWETWA 631
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RESULT 9
I61358
3',5'-cyclic-nucleotide phosphodiesterase (EC 3.1.4.17) 4D, cAMP-specific - human
N;Alternate names: 3',5'-cyclic-AMP phosphodiesterase, rolipram-sensitive
C;Species: Homo sapiens (man)
C;Date: 06-Sep-1996 #sequence_revision 06-Sep-1996 #text_change 17-Nov-2000
C;Accession: I61358; I38416
R;Bolger, G.; Michaeli, T.; Martins, T.; St. John, T.; Steiner, B.; Rodgers, L.; Riggs,
Mol. Cell. Biol. 13, 6558-6571, 1993
A;Title: A family of human phosphodiesterases homologous to the dunce learning and memor
A;Reference number: A54442; MUID:94019330; PMID:8413254
A;Accession: I61358
A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-673 <RES>
A;Cross-references: GB:L20970; NID:g347129; PIDN:AAA03592.1; PID:g347130
R;Baecker, P.A.; Obernolte, R.; Bach, C.; Yee, C.; Shelton, E.R.
Gene 138, 253-256, 1994
A;Title: Isolation of a cDNA encoding a human rolipram-sensitive cyclic AMP phosphodiest
A;Reference number: I38416; MUID:94171048; PMID:8125310
A;Accession: I38416
A;Molecule type: mRNA
A;Residues: 70-507,'P',509-673 <RE2>
A;Cross-references: EMBL:U02882; NID:g433346; PIDN:AAC13745.1; PID:g433347
C;Genetics:
A;Gene: GDB:PDE4D; DPDE3
A;Cross-references: GDB:132541; OMIM:600129
A;Map position: 5q12-5q12
C;Superfamily: 3',5'-cyclic-nucleotide phosphodiesterase 1B, calmodulin-dependent; 3',5'
C;Keywords: cAMP binding; phosphoric diester hydrolase
F;325-553/Domain: 3',5'-cyclic-nucleotide phosphodiesterase homology <CNPD>

Query Match 24.2%; Score 542; DB 2; Length 673;
Best Local Similarity 31.6%; Pred. No. 1.5e-36;
Matches 122; Conservative 82; Mismatches 150; Indels 32; Gaps 7;

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Qy          8 RMLGDVRVRSRAGFESERRGSHPYIDFRIFHSQSEIEV--------SVSARNIRRLLSFQ 59
              | |  :   ||:| :     |: ::|      | |:|:            | : ::   :
Db        178 RELTHLSEMSRSGNQVSEFISNTFLD-----KQHEVEIPSPTQKEKEKKKRPMSQISGVK 232

Qy         60 RYLRSSRFFRGTAVSNS----LNILDDDYNGQAKCMLEKVGNWNFDIFLFDRLTNGNSLV 115
               : : ||      :::|||      :  :  :  ||  || |  |   :|    |:    |
Db        233 KLMHSS------SLTNSSIPRFGVKTEQEDVLAK-ELEDVNKWGLHVFRIAELSGNRPLT 285

Qy        116 SLTFHLFSLHGLIEYFHLDMMKLRRFLVMIQEDYHSQNPYHNAVHAADVTQAMHCYLKEP 175
              :  :|    |:: | : :  |  :|: ::: ||:   ||| :||||| |: |  |  |
Db        286 VIMHTIFQERDLLKTFKIPVDTLITYLMTLEDHYHADVAYHNNIHAADVVQSTHVLLSTP 345

Qy        176 KLANSVTPWDILLSLIAAATHDLDHPGVNQPFLIKTNHYLATLYKNTSVLENHHWRSAVG 235
              |    |  :|| :: |:| ||:|||||:  ||| ||  || :| ::|||||||
Db        346 ALEAVFTDLEILAAIFASAIHDVDHPGVSNQFLINTNSELALMYNDSSVLENHHLAVGFK 405

Qy        236 LLRESG--LFSHLPLESRQQMETQIGALILATDISRQNEYLSLFRSHLD------RGDLC 287
              ||:|    :| :|  : || :   :  ::||||:|:    |:  :: ::       | |
Db        406 LLQEENCDIFQNLTKKQRQSLRKMVIDIVLATDMSKHMNLLADLKTMVETKKVTSSGVLL 465

Qy        288 LEDTRHRHLVLQMALKCADICNPCRTWELSKQWSEKVTEEFFHQGDIEKKYHLGVSPLCD 347
              |::   |  |||  : |||: || :  :| :||:::: |||| ||| |::  : :||:||
Db        466 LDNYSDRIQVLQNMVHCADLSNPTKPLQLYRQWTDRIMEEFFRQGDRERERGMEISPMCD 525

Qy        348 RHTESIANIQIGFMTYLVEPLFTEWA 373
              :|  |:   |:||: |:| ||:  ||
Db        526 KHNASVEKSQVGFIDYIVHPLWETWA 551
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RESULT 10
A54442
3',5'-cyclic-nucleotide phosphodiesterase (EC 3.1.4.17) 4A, cAMP-specific, long splice f
N;Contains: 3',5'-cyclic AMP phosphodiesterase HPDE4A6 splice form
C;Species: Homo sapiens (man)
C;Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 21-Jul-2000
C;Accession: A54442; S55788; A36317; S55787
R;Bolger, G.; Michaeli, T.; Martins, T.; St. John, T.; Steiner, B.; Rodgers, L.; Riggs,
Mol. Cell. Biol. 13, 6558-6571, 1993
A;Title: A family of human phosphodiesterases homologous to the dunce learning and memc
A;Reference number: A54442; MUID:94019330; PMID:8413254
A;Accession: A54442
A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-886 <RES>
A;Cross-references: GB:L20965; NID:g347119; PIDN:AAA03588.1; PID:g347120
R;Sullivan, M.; Egerton, M.; Shakur, Y.; Marquardsen, A.; Houslay, M.D.
Cell. Signal. 6, 793-812, 1994
A;Title: Molecular cloning and expression, in both COS-1 cells and S. cerevisiae, of a
A;Reference number: S55788; MUID:95194817; PMID:7888306
A;Accession: S55788
A;Molecule type: mRNA
A;Residues: 'MCPFPVTTV',210-735,'E',737-886 <SUL>
A;Cross-references: EMBL:U18087; NID:g604374; PIDN:AAC50458.1; PID:g604375
A;Note: 736-Ala was also found
R;Livi, G.P.; Kmetz, P.; McHale, M.M.; Cieslinski, L.B.; Sathe, G.M.; Taylor, D.P.; Dav
Mol. Cell. Biol. 10, 2678-2686, 1990
A;Title: Cloning and expression of cDNA for a human low-K-m, rolipram-sensitive cyclic
A;Reference number: A36317; MUID:90258854; PMID:2160582
A;Accession: A36317
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 'MCPFPVTTV',210-516,'Y',518-722,'R',724-726,'R',728-735,'E',737-788,'E',790
A;Cross-references: GB:M37744
C;Genetics:
A;Gene: GDB:PDE4A; DPDE2
A;Cross-references: GDB:138776; OMIM:600126
A;Map position: 19p13.1-19q12
C;Superfamily: 3',5'-cyclic-nucleotide phosphodiesterase homology
C;Keywords: alternative splicing; cAMP binding; phosphoric diester hydrolase
F;432-660/Domain: 3',5'-cyclic-nucleotide phosphodiesterase homology <CNP>

Query Match 24.1%; Score 541; DB 2; Length 886;
Best Local Similarity 32.3%; Pred. No. 2.6e-36;
Matches 124; Conservative 69; Mismatches 159; Indels 32; Gaps 6;

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Qy         22 ESERRGSH--PYIDFRIFHSQSEIEVSVSARNIRRLLSFQR-----------YLRSSRF 67
              |  | |:    ||       |:|:|:       |      |           :|:
Db        275 EMSRSGNQVSEYISTTFLDKQNEVEIPSPTMKEREKQQAPRPRPSQPPPPPVPHLQPMSQ 334

Qy         68 FRGTAV---SNSLNI-------LDDDYNGQAKCMLEKVGNWNFDIFLFDRLTNGNSLVSL 117
              |       |||||         :  |          || :  |  :||        | ||  :
Db        335 ITGLKKLMHSNSLNNSNIPRFGVKTDQEELLAQELENLNKWGLNIFCVSDYAGGRSLTCI 394

Qy        118 TFHLFSLHGLIEYFHLDMMKLRRFLVMIQEDYHSQNPYHNAVHAADVTQAMHCYLKEPKL 177
               : :|    |:: | : :  :  ::: ::: ||:   |||::||||| |: |  |  | |
Db        395 MYMIFQERDLLKKFRIPVDTMVTYMLTLEDHYHADVAYHNSLHAADVLQSTHVLLATPAL 454

Qy        178 ANSVTPWDILLSLIAAATHDLDHPGVNQPFLIKTNHYLATLYKNTSVLENHHWRSAVGLL 237
                 | :|| :| ||| ||:|||||:  ||| ||  || :| : |||||||      ||
Db        455 DAVFTDLEILAALFAAAIHDVDHPGVSNQFLINTNSELALMYNDESVLENHHLAVGFKLL 514

Qy        238 RESG--LFSHLPLESRQQMETQIGALILATDISRQNEYLSLFRSHLD------RGDLCLE 289
              :|    :| :|    || :   :  ::||||:|:    |:  :: ::       | | |:
Db        515 QEDNCDIFQNLSKRQRQSLRKMVIDMVLATDMSKHMTLLADLKTMVETKKVTSSGVLLLD 574

Qy        290 DTRHRHLVLQMALKCADICNPCRTWELSKQWSEKVTEEFFHQGDIEKKYHLGVSPLCDRH 349
              :  | ||:  : |||: || :  || :||:::: |||| ||| |::  : :||:||:|
Db        575 NYSDRIQVLRNMVHCADLSNPTKPLELYRQWTDRIMAEFFQQGDRERERGMEISPMCDKH 634

Qy        350 TESIANIQIGFMTYLVEPLFTEWA 373
              | |:   |:||: |:| ||:  ||
Db        635 TASVEKSQVGFIDYIVHPLWETWA 658
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RESULT 11
B53109
3',5'-cyclic-nucleotide phosphodiesterase (EC 3.1.4.17) 4B, cAMP-specific, splice form

```
C;Species: Rattus norvegicus (Norway rat)
C;Date: 07-Jul-1995 #sequence_revision 07-Jul-1995 #text_change 19-May-2000
C;Accession: B53109; A34414; C33904; I67944
R;Monaco, L.; Vicini, E.; Conti, M.
J. Biol. Chem. 269, 347-357, 1994
A;Title: Structure of two rat genes coding for closely related rolipram-sensitive cAMP p
A;Reference number: A53109; MUID:94103234; PMID:8276818
A;Accession: B53109
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-584 <MON>
A;Cross-references: GB:U01280
R;Swinnen, J.V.; Joseph, D.R.; Conti, M.
Proc. Natl. Acad. Sci. U.S.A. 86, 8197-8201, 1989
A;Title: The mRNA encoding a high-affinity cAMP phosphodiesterase is regulated by hormon
A;Reference number: A34414; MUID:90046763; PMID:2554303
A;Accession: A34414
A;Molecule type: mRNA
A;Residues: 1-584 <SWI>
A;Cross-references: GB:U09455; GB:M25349; NID:g517501; PIDN:AAA20401.1; PID:g517502; GB:
R;Swinnen, J.V.; Joseph, D.R.; Conti, M.
Proc. Natl. Acad. Sci. U.S.A. 86, 5325-5329, 1989
A;Title: Molecular cloning of rat homologues of the Drosophila melanogaster dunce cAMP p
A;Reference number: A33904; MUID:89315790; PMID:2546153
A;Accession: C33904
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 214-480 <SW2>
A;Cross-references: GB:M25349
R;Bolger, G.B.; Rodgers, L.K.; Riggs, M.
Gene 149, 237-244, 1994
A;Title: Differential CNS expression of alternative mRNA isoforms of the mammalian genes
A;Reference number: I53865; MUID:95047482; PMID:7958996
A;Accession: I67944
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 'EFPGES',34-421,'E',423-584 <RES>
A;Cross-references: GB:L27060; NID:g436009; PID:g436010
C;Superfamily: 3',5'-cyclic-nucleotide phosphodiesterase 1B, calmodulin-dependent; 3',5'
C;Keywords: alternative initiators; alternative splicing; cAMP binding; phosphoric diest
F;237-465/Domain: 3',5'-cyclic-nucleotide phosphodiesterase homology <CNP>

  Query Match             24.0%;  Score 539;  DB 2;  Length 584;
  Best Local Similarity   31.6%;  Pred. No. 2.1e-36;
  Matches  122;  Conservative   81;  Mismatches  151;  Indels   32;  Gaps    7;

Qy          8 RMLGDVRVRSRAGFESERRGSHPYIDFRIFHSQSEIEV--------SVSARNIRRLLSFQ 59
              | |  :   ||:| :     |: ::|      | |:|:           | : ::   :
Db         90 RELTHLSEMSRSGNQVSEYISNTFLD-----KQHEVEIPSPTQKEKEKKKRPMSQISGVK 144

Qy         60 RYLRSSRFFRGTAVSNS----LNILDDDYNGQAKCMLEKVGNWNFDIFLFDRLTNGNSLV 115
             : : ||      :::||      :  :  :  ||  || |  |   :|    |:    |
Db        145 KLMHSS------SLTNSCIPRFGVKTEQEDVLAK-ELEDVNKWGLHVFRIAELSGNRPLT 197

Qy        116 SLTFHLFSLHGLIEYFHLDMMKLRRFLVMIQEDYHSQNPYHNAVHAADVTQAMHCYLKEP 175
              :   :|    |:: | : :  |  :|: ::: ||:   ||| :||||| |: |  | |
Db        198 VIMHTIFQERDLLKTFKIPVDTLITYLMTLEDHYHADVAYHNNIHAADVVQSTHVLLSTP 257

Qy        176 KLANSVTPWDILLSLIAAATHDLDHPGVNQPFLIKTNHYLATLYKNTSVLENHHWRSAVG 235
              |    |  :|| :: |:| ||:|||||:  ||| ||  || :| ::|||||||
Db        258 ALEAVFTDLEILAAIFASAIHDVDHPGVSNQFLINTNSELALMYNDSSVLENHHLAVGFK 317

Qy        236 LLRESG--LFSHLPLESRQQMETQIGALILATDISRQNEYLSLFRSHLD------RGDLC 287
              ||:|    :| :|  : || :      ::||||:|:    |:  :: ::       | |
Db        318 LLQEENCDIFQNLTKKQRQSLRKMAIDIVLATDMSKHMNLLADLKTMVETKKVTSSGVLL 377

Qy        288 LEDTRHRHLVLQMALKCADICNPCRTWELSKQWSEKVTEEFFHQGDIEKKYHLGVSPLCD 347
              |::   |  |||  : |||: || :  :| :||:::: |||| ||| |::  : :||:||
Db        378 LDNYSDRIQVLQNMVHCADLSNPTKPLQLYRQWTDRIMEEFFRQGDRERERGMEISPMCD 437

Qy        348 RHTESIANIQIGFMTYLVEPLFTEWA 373
              :|  |:   |:||: |:| ||:  ||
Db        438 KHNASVEKSQVGFIDYIVHPLWETWA 463
```

```
RESULT 12
I61259
3',5'-cyclic-nucleotide phosphodiesterase (EC 3.1.4.17) 4D, cAMP-specific, splice form
N;Alternate names: cyclic-AMP phosphodiesterase
N;Contains: 3',5'-cyclic-nucleotide phosphodiesterase (EC 3.1.4.17) 4D, cAMP-specific,
C;Species: Rattus norvegicus (Norway rat)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 17-Nov-2000
C;Accession: I61259; A53678; I67943
R;Sette, C.; Vicini, E.; Conti, M.
J. Biol. Chem. 269, 18271-18274, 1994
A;Title: The ratPDE3/IVd phosphodiesterase gene codes for multiple proteins differentia
A;Reference number: A53678; MUID:94308045; PMID:8034568
A;Accession: I61259
A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-672 <RES>
A;Cross-references: EMBL:U09457; NID:g517418; PID:g517419
A;Accession: A53678
A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 167-672 <RE2>
A;Cross-references: EMBL:U09456; NID:g517416; PIDN:AAA20393.1; PID:g517417
R;Bolger, G.B.; Rodgers, L.K.; Riggs, M.
Gene 149, 237-244, 1994
A;Title: Differential CNS expression of alternative mRNA isoforms of the mammalian gene
A;Reference number: I53865; MUID:95047482; PMID:7958996
A;Accession: I67943
A;Status: translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 'N',96-625,'Y',627-672 <RE3>
A;Cross-references: GB:L27059; NID:g436007; PIDN:AAA56857.1; PID:g436008
C;Genetics:
A;Gene: PDE3/IVd gene
C;Superfamily: 3',5'-cyclic-nucleotide phosphodiesterase 1B, calmodulin-dependent; 3',!
C;Keywords: cAMP binding; phosphoric diester hydrolase
F;325-553/Domain: 3',5'-cyclic-nucleotide phosphodiesterase homology <CNP>

  Query Match             24.0%;  Score 539;  DB 2;  Length 672;
  Best Local Similarity   31.6%;  Pred. No. 2.6e-36;
  Matches  122;  Conservative   81;  Mismatches  151;  Indels   32;  Gaps    7;

Qy          8 RMLGDVRVRSRAGFESERRGSHPYIDFRIFHSQSEIEV--------SVSARNIRRLLSFQ 59
              | |  :   ||:| :     |: ::|      | |:|:           | : ::   :
Db        178 RELTHLSEMSRSGNQVSEYISNTFLD-----KQHEVEIPSPTQKEKEKKKRPMSQISGVK 232

Qy         60 RYLRSSRFFRGTAVSNS----LNILDDDYNGQAKCMLEKVGNWNFDIFLFDRLTNGNSLV 115
             : : ||      :::||      :  :  :  ||  || |  |   :|    |:    |
Db        233 KLMHSS------SLTNSCIPRFGVKTEQEDVLAK-ELEDVNKWGLHVFRIAELSGNRPLT 285

Qy        116 SLTFHLFSLHGLIEYFHLDMMKLRRFLVMIQEDYHSQNPYHNAVHAADVTQAMHCYLKEP 175
              :   :|    |:: | : :  |  :|: ::: ||:   ||| :||||| |: |  | |
Db        286 VIMHTIFQERDLLKTFKIPVDTLITYLMTLEDHYHADVAYHNNIHAADVVQSTHVLLSTP 345

Qy        176 KLANSVTPWDILLSLIAAATHDLDHPGVNQPFLIKTNHYLATLYKNTSVLENHHWRSAVG 235
              |    |  :|| :: |:| ||:|||||:  ||| ||  || :| ::|||||||
Db        346 ALEAVFTDLEILAAIFASAIHDVDHPGVSNQFLINTNSELALMYNDSSVLENHHLAVGFK 405

Qy        236 LLRESG--LFSHLPLESRQQMETQIGALILATDISRQNEYLSLFRSHLD------RGDLC 287
              ||:|    :| :|  : || :      ::||||:|:    |:  :: ::       | |
Db        406 LLQEENCDIFQNLTKKQRQSLRKMAIDIVLATDMSKHMNLLADLKTMVETKKVTSSGVLL 465

Qy        288 LEDTRHRHLVLQMALKCADICNPCRTWELSKQWSEKVTEEFFHQGDIEKKYHLGVSPLCD 347
              |::   |  |||  : |||: || :  :| :||:::: |||| ||| |::  : :||:||
Db        466 LDNYSDRIQVLQNMVHCADLSNPTKPLQLYRQWTDRIMEEFFRQGDRERERGMEISPMCD 525

Qy        348 RHTESIANIQIGFMTYLVEPLFTEWA 373
              :|  |:   |:||: |:| ||:  ||
Db        526 KHNASVEKSQVGFIDYIVHPLWETWA 551


RESULT 13
```

S71626
3',5'-cyclic-nucleotide phosphodiesterase (EC 3.1.4.17), cAMP-specific - human
N;Alternate names: 3',5'-cyclic AMP phosphodiesterase
C;Species: Homo sapiens (man)
C;Date: 27-Nov-1997 #sequence_revision 12-Dec-1997 #text_change 17-Nov-2000
C;Accession: S71626; I61356
R;Engels, P.; Sullivan, M.; Mueller, T.; Luebbert, H.
FEBS Lett. 358, 305-310, 1995
A;Title: Molecular cloning and functional expression in yeast of a human cAMP-specific p
A;Reference number: S71626; MUID:95145731; PMID:7843419
A;Accession: S71626
A;Molecule type: DNA
A;Residues: 1-712 <ENG>
A;Cross-references: EMBL:Z46632; NID:g727222; PIDN:CAA86601.1; PID:g727223
A;Experimental source: substantia nigra
R;Bolger, G.; Michaeli, T.; Martins, T.; St. John, T.; Steiner, B.; Rodgers, L.; Riggs,
Mol. Cell. Biol. 13, 6558-6571, 1993
A;Title: A family of human phosphodiesterases homologous to the dunce learning and memor
A;Reference number: A54442; MUID:94019330; PMID:8413254
A;Accession: I61356
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 462-712 <RES>
A;Cross-references: GB:L20968; NID:g347125; PIDN:AAA03591.1; PID:g347126
C;Genetics:
A;Gene: HSPDE4C1
C;Function:
A;Description: cAMP hydrolysis; converts cAMP to non-cyclic AMP
A;Pathway: cyclic nucleotide metabolism
A;Note: expressed in various tissues but not in cells of the immune system
C;Superfamily: 3',5'-cyclic-nucleotide phosphodiesterase 1B, calmodulin-dependent; 3',5'
C;Keywords: phosphoric diester hydrolase
F;387-615/Domain: 3',5'-cyclic-nucleotide phosphodiesterase homology <CNP>

Query Match 23.9%; Score 536; DB 2; Length 712;
Best Local Similarity 33.2%; Pred. No. 5e-36;
Matches 123; Conservative 70; Mismatches 153; Indels 24; Gaps 7;

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Qy          22 ESERRGSH--PYIDFRIFHSQSEIEV-SVSARNIRRLLSFQRYLRSSRFFRGTAVSNSLN 78
               |: | |:    ||      |:|:|:  |:|    : :|     | |    |   | ||:
Db         250 ETSRSGNQVSEYISRTFLDQQTEVELPKVTAEEAPQPMS-----RISG-LHGLCHSASLS 303

Qy          79 I-------LDDDYNGQAKCMLEKVGNWNFDIFLFDRLTNGNSLVSLTFHLFSLHGLIEYF 131
                     :  |    |     ||     |  |:|    ::    | :: | :|    |:: |
Db         304 SATVPRFGVQTDQEEQLAKELEDTNKWGLDVFKVADVSGNRPLTAIIFSIFQERDLLKTF 363

Qy         132 HLDMMKLRRFLVMIQEDYHSQNPYHNAVHAADVTQAMHCYLKEPKLANSVTPWDILLSLI 191
                :    |  :|:|::  ||:   |||::|||||  |: |  |  | |     |  :|| :|
Db         364 QIPADTLATYLLMLEGHYHANVAYHNSLHAADVAQSTHVLLATPALEAVFTDLEILAALF 423

Qy         192 AAATHDLDHPGVNQPFLIKTNHYLATLYKNTSVLENHHWRSAVGLLRESG--LFSHLPLE 249
               |:| ||:|||||:  ||| ||  :| :| : ||||||     ||:    :| :|  :
Db         424 ASAIHDVDHPGVSNQFLINTNSDVALMYNDASVLENHHLAVGFKLLQAENCDIFQNLSAK 483

Qy         250 SRQQMETQIGALILATDISRQNEYLSLFRSHLDR------GDLCLEDTRHRHLVLQMALK 303
                |  :   :  ::|||:|:    |:  :: ::      | | |::   |  |||  :
Db         484 QRLSLRRMVIDMVLATDMSKHMNLLADLKTMVETKKVTSLGVLLLDNYSDRIQVLQNLVH 543

Qy         304 CADICNPCRTWELSKQWSEKVTEEFFHQGDIEKKYHLGVSPLCDRHTESIANIQIGFMTY 363
               |||: || :   | :||:::  ||| ||| |::  | :||:||:|| |:   |:||: |
Db         544 CADLSNPTKPLPLYRQWTDRIMAEFFQQGDRERESGLDISPMCDKHTASVEKSQVGFIDY 603

Qy         364 LVEPLFTEWA 373
               :  ||:  ||
Db         604 IAHPLWETWA 613
```

RESULT 14
I67945
3',5'-cyclic-nucleotide phosphodiesterase (EC 3.1.4.17) - rat (fragment)
N;Alternate names: cAMP phosphodiesterase 1
C;Species: Rattus norvegicus (Norway rat)
C;Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 03-Nov-2000
C;Accession: I67945; A33904
R;Bolger, G.B.; Rodgers, L.K.; Riggs, M.
Gene 149, 237-244, 1994
A;Title: Differential CNS expression of alternative mRNA isoforms of the mammalian gene
A;Reference number: I53865; MUID:95047482; PMID:7958996
A;Accession: I67945
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-536 <RES>
A;Cross-references: GB:L27061; NID:g436011; PIDN:AAA56858.1; PID:g436012
R;Swinnen, J.V.; Joseph, D.R.; Conti, M.
Proc. Natl. Acad. Sci. U.S.A. 86, 5325-5329, 1989
A;Title: Molecular cloning of rat homologues of the Drosophila melanogaster dunce cAMP
A;Reference number: A33904; MUID:89315790; PMID:2546153
A;Accession: A33904
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 230-496 <SWI>
A;Cross-references: GB:M25347; GB:M28410
C;Superfamily: 3',5'-cyclic-nucleotide phosphodiesterase 1B, calmodulin-dependent; 3',5
C;Keywords: alternative splicing; cAMP binding; phosphoric diester hydrolase
F;253-481/Domain: 3',5'-cyclic-nucleotide phosphodiesterase homology <CNPD>

Query Match 23.8%; Score 534.5; DB 2; Length 536;
Best Local Similarity 32.2%; Pred. No. 4.5e-36;
Matches 118; Conservative 71; Mismatches 159; Indels 19; Gaps 6;

```
Qy          22 ESERRGSH--PYIDFRIFHSQSEIEVSVSARN-----IRRLLSFQRYLRSSRFFRGTAVS 74
               |: | |:    ||      |:|:|:          : ::   ::   :|     ||
Db         117 ETSRSGNQVSEYISQTFLDQQAEVELPAPPTEDHPWPMAQITGLRKSCHTS---LPTAAI 173

Qy          75 NSLNILDDDYNGQAKCMLEKVGNWNFDIFLFDRLTNGNSLVSLTFHLFSLHGLIEYFHLD 134
                  :  |     ||  ||     |  |:|    |:    | :: | :    |:: | :
Db         174 PRFGVQTDQEEQLAK-ELEDTNKWGLDVFKVAELSGNRPLTAVIFRVLQERDLLKTFQIP 232

Qy         135 MMKLRRFLVMIQEDYHSQNPYHNAVHAADVTQAMHCYLKEPKLANSVTPWDILLSLIAAA 194
                  | |:|: ::  |||   |||::|||||  |: |  |  | |     |  ::| :: | |
Db         233 ADTLLRYLLTLEGHYHSNVAYHNSIHAADVVQSAHVLLGTPALEAVFTDLEVLAAIFACA 292

Qy         195 THDLDHPGVNQPFLIKTNHYLATLYKNTSVLENHHWRSAVGLLR--ESGLFSHLPLESRQ 252
                  ||:|||||:  |||  ||  || :| ::|||||||      ||:     :| :|  : :
Db         293 IHDVDHPGVSNQFLINTNSELALMYNDSSVLENHHLAVGFKLLQGENCDIFQNLSTKQKL 352

Qy         253 QMETQIGALILATDISRQNEYLSLFRSHLDR------GDLCLEDTRHRHLVLQMALKCAD 306
                  :   :  ::|||:|:    |:  :: ::      | | |::   |  |||  : |||
Db         353 SLRRMVIDMVLATDMSKHMSLLADLKTMVETKKVTSLGVLLLDNYSDRIQVLQSLVHCAD 412

Qy         307 ICNPCRTWELSKQWSEKVTEEFFHQGDIEKKYHLGVSPLCDRHTESIANIQIGFMTYLVE 366
               : || :   | :||:|::  ||| ||| |::  | :||:||:|| |:   |:||: |:
Db         413 LSNPAKPLPLYRQWTERIMAEFFQQGDRERESGLDISPMCDKHTASVEKSQVGFIDYIAH 472

Qy         367 PLFTEWA 373
               ||:  ||
Db         473 PLWETWA 479
```

RESULT 15
JW0088
3',5'-cyclic-nucleotide phosphodiesterase (EC 3.1.4.17) 8A, high affinity cAMP-specifi
N;Alternate names: high affinity cAMP-specific phosphodiesterase PDE8A
C;Species: Homo sapiens (man)
C;Date: 18-Jun-1998 #sequence_revision 26-Aug-1999 #text_change 21-Jul-2000
C;Accession: JW0088
R;Fisher, D.A.; Smith, J.F.; Pillar, J.S.; St Denis, S.H.; Cheng, J.B.
Biochem. Biophys. Res. Commun. 246, 570-577, 1998
A;Title: Isolation and characterization of PDE8A, a novel human cAMP-specific phosphod
A;Reference number: JW0088; MUID:98289571; PMID:9618252
A;Accession: JW0088
A;Molecule type: mRNA
A;Residues: 1-713 <FIS>
A;Cross-references: GB:AF056490; NID:g3184388; PIDN:AAC39763.1; PID:g3184389
C;Superfamily: 3',5'-cyclic-nucleotide phosphodiesterase 8A, high affinity cAMP-specif
C;Keywords: alternative splicing; cAMP binding; phosphoric diester hydrolase

F;439-680/Domain: 3',5'-cyclic-nucleotide phosphodiesterase homology <CNPD>

Query Match 22.4%; Score 503; DB 2; Length 713;
Best Local Similarity 31.6%; Pred. No. 2.6e-33;
Matches 117; Conservative 76; Mismatches 145; Indels 32; Gaps 7;

```
Qy          54 RLLSFQRYLRSSRFFRGTAVSNSLNILD----DDYNGQAKCMLEKVGNWNFDIFLFDRLT 109
               | ||   |: |:   : | : :| ||:     ||   :    :|    |:||||  :  |
Db         338 RRLSGNEYVLST---KNTQMVSS-NIITPISLDDVPPRIARAMENEEYWDFDIFELEAAT 393

Qy         110 NGNSLVSLTFHLFSLHGLIEYFHLDMMKLRRFLVMIQEDYHSQNPYHNAVHAADVTQAMH 169
               :   |: |   :|:  |: |: |      || :| :|: :||| |||||: |:|||  |
Db         394 HNRPLIYLGLKMFARFGICEFLHCSESTLRSWLQIIEANYHSSNPYHNSTHSADVLHATA 453

Qy         170 CYLKEPKLANSVTPWDILLSLIAAATHDLDHPGVNQPFLIKTNHYLATLYKNTSVLENHH 229
               :| : ::  :: | | : :|||| ||:|||| ||      || || :|:|||:||
Db         454 YFLSKERIKETLDPIDEVAALIAATIHDVDHPGRTNSFLCNAGSELAILYNDTAVLESHH 513

Qy         230 WRSAVGLLR---ESGLFSHLPLESRQQMETQIGALILATDISRQNEYLSLFRSHLDRGDL 286
               |  |     :  :| :: ·   : :   |  ::|||:::: |::: | : :::
Db         514 AALAFQLTTGDDKCNIFKNMERNDYRTLRQGIIDMVLATEMTKHFEHVNKFVNSINKPLA 573

Qy         287 CLEDT----------------RHRHLVLQMALKCADICNPCRTWELSKQWSEKVTEEFF 329
               ||:                  :| |: :| :|||: |||  :   :|: :::||:|
Db         574 TLEENGETDKNQEVINTMLRTPENRTLIKRMLIKCADVSNPCRPLQYCIEWAARISEEYF 633

Qy         330 HQGDIEKKYHLG-VSPLCDRHTESIANIQIGFMTYLVEPLFTEWARFSNTRLSQTMLGHV 388
               | | ||:  |  | |: ||:| ||   || |: | :  :|  |  | :       :: |:
Db         634 SQTDEEKQQGLPVVMPVFDRNTCSIPKSQISFIDYFITDMFDAWDAFVDL---PDLMQHL 690

Qy         389 GLNKASWKGL 398
               |   ||||
Db         691 DNNFKYWKGL 700
```

Search completed: May 26, 2004, 09:25:36
Job time : 22 secs

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: May 26, 2004, 09:24:28 ; Search time 46 Seconds
(without alignments)
2921.973 Million cell updates/sec

Title: US-09-966-781A-1
Perfect score: 2243
Sequence: 1 DQTALYIRMLGDVRVRSRAG.....DTDAAFELNSQLLPQENRLS 426

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL_25:*
1: sp_archea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_rvirus:*
16: sp_bacteriap:*
17: sp_archeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1910	85.2	424	4	Q96T72	Q96t72 homo sapien
2	1389.5	61.9	446	11	Q8VIE4	Q8vie4 rattus norv
3	1377.5	61.4	422	4	Q9BZ40	Q9bz40 homo sapien
4	1377.5	61.4	446	11	Q8CBS2	Q8cbs2 mus musculu
5	1377.5	61.4	459	11	Q8VIE2	Q8vie2 rattus norv
6	1231.5	54.9	359	11	Q8VIE3	Q8vie3 rattus norv
7	717	32.0	162	4	Q86V65	Q86v65 homo sapien
8	555	24.7	771	11	Q9EQR7	Q9eqr7 rattus norv
9	551	24.6	721	11	Q9QXI7	Q9qxi7 mus musculu
10	550	24.5	542	11	Q91VY2	Q91vy2 mus musculu
11	550	24.5	606	4	Q13945	Q13945 homo sapien
12	550	24.5	659	11	Q8VD81	Q8vd81 rattus norv
13	550	24.5	721	11	Q8VBU5	Q8vbu5 mus musculu
14	550	24.5	736	11	Q8VD82	Q8vd82 rattus norv
15	548	24.4	687	4	Q8IV84	Q8iv84 homo sapien
16	545	24.3	518	4	O43850	O43850 homo sapien
17	545	24.3	700	4	P78505	P78505 homo sapien
18	545	24.3	782	4	O76105	O76105 homo sapien
19	545	24.3	791	4	O43849	O43849 homo sapien
20	543	24.2	584	11	Q8C4Q7	Q8c4q7 mus musculu
21	543	24.2	747	11	Q8CG05	Q8cg05 mus musculu
22	542	24.2	518	4	Q8IVD3	Q8ivd3 homo sapien
23	542	24.2	679	4	Q7Z2L8	Q7z2l8 homo sapien
24	542	24.2	748	4	Q8IVD2	Q8ivd2 homo sapien
25	541	24.1	647	4	Q8IVA7	Q8iva7 homo sapien
26	541	24.1	825	4	Q9H3H2	Q9h3h2 homo sapien
27	539	24.0	517	11	Q8CG06	Q8cg06 rattus norv
28	539	24.0	747	11	Q8CG04	Q8cg04 rattus norv
29	539	24.0	803	11	O35470	O35470 rattus norv
30	538	24.0	518	4	Q8IVA9	Q8iva9 homo sapien
31	535	23.9	426	4	Q9UPJ5	Q9upj5 homo sapien
32	503	22.4	829	4	Q96T71	Q96t71 homo sapien
33	500	22.3	383	11	Q8BQB2	Q8bqb2 mus musculu
34	493.5	22.0	599	5	Q8IFZ3	Q8ifz3 caenorhabdi
35	493.5	22.0	612	5	Q86NE9	Q86ne9 caenorhabdi
36	493.5	22.0	626	5	Q95ZQ6	Q95zq6 caenorhabdi
37	493.5	22.0	674	5	Q86NE8	Q86ne8 caenorhabdi
38	478	21.3	521	5	Q8MRN3	Q8mrn3 drosophila
39	478	21.3	624	5	Q9W4S8	Q9w4s8 drosophila
40	478	21.3	629	5	Q8IRU5	Q8iru5 drosophila
41	478	21.3	642	5	Q8IRU6	Q8iru6 drosophila
42	478	21.3	662	5	Q8IRU4	Q8iru4 drosophila
43	478	21.3	711	5	Q8IRU7	Q8iru7 drosophila
44	478	21.3	776	5	Q8IRU8	Q8iru8 drosophila
45	478	21.3	778	5	Q8IRU9	Q8iru9 drosophila

ALIGNMENTS

RESULT 1
Q96T72
ID Q96T72 PRELIMINARY; PRT; 424 AA.
AC Q96T72;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE cAMP-specific cyclic nucleotide phosphodiesterase PDE7A3.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21265467; PubMed=11371644;
RA Glavas N.A., Ostenson C., Schaefer J.B., Vasta V., Beavo J.A.;
RT "T cell activation up-regulates cyclic nucleotide phosphodiesterases
RT 8A1 and 7A3.";
RL Proc. Natl. Acad. Sci. U.S.A. 98:6319-6324(2001).
DR EMBL; AF332652; AAK57640.1; -.
DR GO; GO:0004114; F:3',5'-cyclic-nucleotide phosphodiesterase a. . .; IEA.
DR GO; GO:0003824; F:catalytic activity; IEA.
DR GO; GO:0007165; P:signal transduction; IEA.
DR InterPro; IPR003607; Met_phsphohydro.
DR InterPro; IPR002073; PDEase.
DR Pfam; PF00233; PDEase; 1.
DR PRINTS; PR00387; PDIESTERASE1.
DR SMART; SM00471; HDc; 1.
DR PROSITE; PS00126; PDEASE_I; 1.
SQ SEQUENCE 424 AA; 48827 MW; A7DBF40D08A7B561 CRC64;

Query Match 85.2%; Score 1910; DB 4; Length 424;
Best Local Similarity 99.5%; Pred. No. 8.4e-164;
Matches 362; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```
Qy          1 DQTALYIRMLGDVRVRSRAGFESERRGSHPYIDFRIFHSQSEIEVSVSARNIRRLLSFQR 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         57 DQTALYIRMLGDVRVRSRAGFESERRGSHPYIDFRIFHSQSEIEVSVSARNIRRLLSFQR 116
```

```
Qy         61 YLRSSRFFRGTAVSNSLNILDDDYNGQAKCMLEKVGNWNFDIFLFDRLTNGNSLVSLTFH 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        117 YLRSSRFFRGTAVSNSLNILDDDYNGQAKCMLEKVGNWNFDIFLFDRLTNGNSLVSLTFH 176

Qy        121 LFSLHGLIEYFHLDMMKLRRFLVMIQEDYHSQNPYHNAVHAADVTQAMHCYLKEPKLANS 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        177 LFSLHGLIEYFHLDMMKLRRFLVMIQEDYHSQNPYHNAVHAADVTQAMHCYLKEPKLANS 236

Qy        181 VTPWDILLSLIAAATHDLDHPGVNQPFLIKTNHYLATLYKNTSVLENHHWRSAVGLLRES 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        237 VTPWDILLSLIAAATHDLDHPGVNQPFLIKTNHYLATLYKNTSVLENHHWRSAVGLLRES 296

Qy        241 GLFSHLPLESRQQMETQIGALILATDISRQNEYLSLFRSHLDRGDLCLEDTRHRHLVLQM 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        297 GLFSHLPLESRQQMETQIGALILATDISRQNEYLSLFRSHLDRGDLCLEDTRHRHLVLQM 356

Qy        301 ALKCADICNPCRTWELSKQWSEKVTEEFFHQGDIEKKYHLGVSPLCDRHTESIANIQIGF 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        357 ALKCADICNPCRTWELSKQWSEKVTEEFFHQGDIEKKYHLGVSPLCDRHTESIANIQIGN 416

Qy        361 MTYL 364
              |||
Db        417 YTYL 420


RESULT 2
Q8VIE4
ID   Q8VIE4      PRELIMINARY;      PRT;   446 AA.
AC   Q8VIE4;
DT   01-MAR-2002 (TrEMBLrel. 20, Created)
DT   01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Cyclic nucleotide phosphodiesterase 7B1 (EC 3.1.4.17).
GN   RNPDE7B.
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Brain;
RA   Sasaki T., Kotera J., Omori K.;
RT   "Novel alternative splice variants of rat PDE7B.";
RL   Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AB057409; BAB79637.1; -.
DR   GO; GO:0004114; F:3',5'-cyclic-nucleotide phosphodiesterase a. . .; IEA.
DR   GO; GO:0016787; F:hydrolase activity; IEA.
DR   GO; GO:0007165; P:signal transduction; IEA.
DR   InterPro; IPR003607; Met_phsphohydro.
DR   InterPro; IPR002073; PDEase.
DR   Pfam; PF00233; PDEase; 1.
DR   SMART; SM00471; HDc; 1.
DR   PROSITE; PS00126; PDEASE_I; 1.
KW   Hydrolase.
SQ   SEQUENCE   446 AA;  51475 MW;  01567BDABC905D19 CRC64;

  Query Match           61.9%;  Score 1389.5;  DB 11;  Length 446;
  Best Local Similarity  62.4%;  Pred. No. 8.9e-117;
  Matches  257;  Conservative   65;  Mismatches   85;  Indels    5;  Gaps    2;

Qy          1 DQTALYIRMLGDVRVRSRAGFESERRGSHPYIDFRIFHSQSEIEVSVSARNIRRLLSFQR 60
              :|    : |||||:| : |  :|||||:|:||||: :: :      | : :||||||||
Db         18 EQNVKCVCMLGDVRLRGQTGVPAERRGSYPFIDFRLLNNTTHSGEIGSKKKVRRLLSFQR 77

Qy         61 YLRSSRFFRGTAVSNSLNILDDDYNGQAKCMLEKVGNWNFDIFLFDRLTNGNSLVSLTFH 120
              :   ||  ||      |::||:|| |||: || ||| |:|||||||||||||:|  |
Db         78 HFHESRLLRGMTPQAPLHLLDEDYLGQARHMLSKVGMWDFDIFLFDRLTNGNSLVTLLCH 137

Qy        121 LFSLHGLIEYFHLDMMKLRRFLVMIQEDYHSQNPYHNAVHAADVTQAMHCYLKEPKLANS 180
              ||: |||| :| |||: | |||||:|||||  |||||||||||||||||||||||||:
Db        138 LFNSHGLIHHFKLDMVTLHRFLVMVQEDYHGHNPYHNAVHAADVTQAMHCYLKEPKLASF 197

Qy        181 VTPWDILLSLIAAATHDLDHPGVNQPFLIKTNHYLATLYKNTSVLENHHWRSAVGLLRES 240
              :|| ||:| |:||| ||:|||||||||||||||||||:|| ||:| ||||||||| :|:|||| 
Db        198 LTPLDIMLGLLAAAAHDVDHPGVNQPFLIKTNHHLANLYQNMSVLENHHWRSTIGMLRES 257

Qy        241 GLFSHLPLESRQQMETQIGALILATDISRQNEYLSLFRSHLDRGDLCLEDTRHRHLVLQM 300
              | :||| |  | :| |:|:|||||||:||||:|:  ::||   || ||: : || :||:
Db        258 RLLAHLPKEMTQDIEQQLGSLILATDINRQNEFLTRLKAHLHNKDLRLENIQDRHFMLQI 317

Qy        301 ALKCADICNPCRTWELSKQWSEKVTEEFFHQGDIEKKYHLGVSPLCDRHTESIANIQIGF 360
              |||||||||||| ||:|||||:| ||| ||||:|:|: | :||||::  :|| :|||||
Db        318 ALKCADICNPCRIWEMSKQWSERVCEEFYRQGDLEQKFELEISPLCNQQKDSIPSIQIGF 377

Qy        361 MTYLVEPLFTEWARFS-NTRLSQTMLGHVGLNKASWKGL----QREQSSSED 407
              |||:||||| |||||: |: ||::|| |:  ||| || |     | : | :|
Db        378 MTYIVEPLFREWARFTGNSTLSESMLNHLAHNKAQWKSLLSNQHRRRGSGQD 429


RESULT 3
Q9BZ40
ID   Q9BZ40      PRELIMINARY;      PRT;   422 AA.
AC   Q9BZ40;
DT   01-JUN-2001 (TrEMBLrel. 17, Created)
DT   01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   BA472E5.1 (High-affinity cAMP-specific 3',5'-cyclic phosphodiesterase
DE   (EC 3.1.4.17, rolipram-insensitive phosphodiesterase type 7))
DE   (Fragment).
GN   BA472E5.1.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Cobley V.;
RL   Submitted (DEC-2000) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AL138828; CAC27545.1; -.
DR   GO; GO:0004114; F:3',5'-cyclic-nucleotide phosphodiesterase a. . .; IEA.
DR   GO; GO:0003824; F:catalytic activity; IEA.
DR   GO; GO:0007165; P:signal transduction; IEA.
DR   InterPro; IPR003607; Met_phsphohydro.
DR   InterPro; IPR002073; PDEase.
DR   Pfam; PF00233; PDEase; 1.
DR   PRINTS; PR00387; PDIESTERASE1.
DR   SMART; SM00471; HDc; 1.
DR   PROSITE; PS00126; PDEASE_I; 1.
FT   NON_TER       1       1
SQ   SEQUENCE   422 AA;  48718 MW;  E5E2637251l9A64D CRC64;

  Query Match           61.4%;  Score 1377.5;  DB 4;  Length 422;
  Best Local Similarity  62.8%;  Pred. No. 1e-115;
  Matches  252;  Conservative   65;  Mismatches   83;  Indels    1;  Gaps    1;

Qy         12 DVRVRSRAGFESERRGSHPYIDFRIFHSQSEIEVSVSARNIRRLLSFQRYLRSSRFFRGT 71
              |:|:| : |  :|||||:|:||||: :| :      : : ::|||||||  :||  ||
Db          1 DIRLRGQTGVRAERRGSYPFIDFRLLNSTTYSGEIGTKKKVKRLLSFQRYFHASRLLRGI 60

Qy         72 AVSNSLNILDDDYNGQAKCMLEKVGNWNFDIFLFDRLTNGNSLVSLTFHLFSLHGLIEYF 131
                 |::||:|| |||: || ||| |:|||||||||||||:|  |||: |||| :|
Db         61 IPQAPLHLLDEDYLGQARHMLSKVGMWDFDIFLFDRLTNGNSLVTLLCHLFNTHGLIHHF 120

Qy        132 HLDMMKLRRFLVMIQEDYHSQNPYHNAVHAADVTQAMHCYLKEPKLANSVTPWDILLSLI 191
              |||: | |||||:|||||||||||||||||||||||||||||||: :|| ||:| |:
Db        121 KLDMVTLHRFLVMVQEDYHSQNPYHNAVHAADVTQAMHCYLKEPKLASFLTPLDIMLGLL 180

Qy        192 AAATHDLDHPGVNQPFLIKTNHYLATLYKNTSVLENHHWRSAVGLLRESGLFSHLPLESR 251
              ||| ||:|||||||||||||:|| ||:| |||||||||| :|:|||| | :||| |
Db        181 AAAAHDVDHPGVNQPFLIKTNHHLANLYQNMSVLENHHWRSTIGMLRESRLLAHLPKEMT 240

Qy        252 QQMETQIGALILATDISRQNEYLSLFRSHLDRGDLCLEDTRHRHLVLQMALKCADICNPC 311
              | :| |:|:|||||||:||||:|:  ::||   || ||| : || :||:||||||||||
Db        241 QDIEQQLGSLILATDINRQNEFLTRLKAHLHNKDLRLEDAQDRHFMLQIALKCADICNPC 300

Qy        312 RTWELSKQWSEKVTEEFFHQGDIEKKYHLGVSPLCDRHTESIANIQIGFMTYLVEPLFTE 371
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Db        301 RIWEMSKQWSERVCEEFYRQGELEQKFELEISPLCNQQKDSIPSIQIGFMSYIVEPLFRE 360

Qy        372 WARFS-NTRLSQTMLGHVGLNKASWKGLQREQSSSEDTDAA 411
Db        361 WAHFTGNSTLSENMLGHLAHNKAQWKSLLPRQHRSRGSSGS 401
```

RESULT 4
Q8CBS2
ID Q8CBS2 PRELIMINARY; PRT; 446 AA.
AC Q8CBS2;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Phosphodiesterase 7B.
GN PDE7B.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Urinary bladder;
RX MEDLINE=22354683; PubMed=12466851;
RA The FANTOM Consortium,
RA the RIKEN Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573(2002).
DR EMBL; AK035385; BAC29052.1; -.
DR MGD; MGI:1352752; Pde7b.
DR GO; GO:0004115; F:cAMP-specific phosphodiesterase activity; IDA.
DR InterPro; IPR003607; Met_phsphohydro.
DR InterPro; IPR002073; PDEase.
DR Pfam; PF00233; PDEase; 1.
DR PRINTS; PR00387; PDIESTERASE1.
DR SMART; SM00471; HDc; 1.
DR PROSITE; PS00126; PDEASE_I; 1.
SQ SEQUENCE 446 AA; 51307 MW; 7C002364B396A5A8 CRC64;

Query Match 61.4%; Score 1377.5; DB 11; Length 446;
Best Local Similarity 61.9%; Pred. No. 1.1e-115;
Matches 255; Conservative 67; Mismatches 85; Indels 5; Gaps 2;

```
Qy          1 DQTALYIRMLGDVRVRSRAGFESERRGSHPYIDFRIFHSQSEIEVSVSARNIRRLLSFQR 60
Db         18 EQSVKCVCMLGDVRLRGQTGVPAERRGSYPFIDFRLLNNTTHSGEIGTKKKVKRLLSFQR 77

Qy         61 YLRSSRFFRGTAVSNSLNILDDDYNGQAKCMLEKVGNWNFDIFLFDRLTNGNSLVSLTFH 120
Db         78 YFHASRLLRGIIPQAPLHLLDEDYLGQARHMLSKVGTWDFDIFLFDRLTNGNSLVTLLCH 137

Qy        121 LFSLHGLIEYFHLDMMKLRRFLVMIQEDYHSQNPYHNAVHAADVTQAMHCYLKEPKLANS 180
Db        138 LFNSHGLIHHFKLDMVTLHRFLVMVQEDYHGHNPYHNAVHAADVTQAMHCYLKEPKLASF 197

Qy        181 VTPWDILLSLIAAATHDLDHPGVNQPFLIKTNHYLATLYKNTSVLENHHWRSAVGLLRES 240
Db        198 LTPLDIMLGLLAAAAHDVDHPGVNQPFLIKTNHHLANLYQNMSVLENHHWRSTIGMLRES 257

Qy        241 GLFSHLPLESRQQMETQIGALILATDISRQNEYLSLFRSHLDRGDLCLEDTRHRHLVLQM 300
Db        258 RLLAHLPKEMTQDIEQQLGSLILATDINRQNEFLTRLKAHLHNKDLRLENVQDRHFMLQI 317

Qy        301 ALKCADICNPCRTWELSKQWSEKVTEEFFHQGDIEKKYHLGVSPLCDRHTESIANIQIGF 360
Db        318 ALKCADICNPCRIWEMSKQWSERVCEEFYRQGDLEQKFELEISPLCNQQKDSIPSIQIGF 377

Qy        361 MTYLVEPLFTEWARFS-NTRLSQTMLGHVGLNKASWKGL----QREQSSSED 407
Db        378 MTYIVEPLFRERARFTGNSTLSENMLSHLAHNKAQWKSLLSNQHRRRGSGQD 429
```

RESULT 5
Q8VIE2
ID Q8VIE2 PRELIMINARY; PRT; 459 AA.
AC Q8VIE2;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Cyclic nucleotide phosphodiesterase 7B4 (EC 3.1.4.17).
GN RNPDE7B.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Skeletal muscle;
RA Sasaki T., Kotera J., Omori K.;
RT "Novel alternative splice variants of rat PDE7B.";
RL Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AB057411; BAB79639.1; -.
DR GO; GO:0004114; F:3',5'-cyclic-nucleotide phosphodiesterase a. . .; IEA.
DR GO; GO:0016787; F:hydrolase activity; IEA.
DR GO; GO:0007165; P:signal transduction; IEA.
DR InterPro; IPR003607; Met_phsphohydro.
DR InterPro; IPR002073; PDEase.
DR Pfam; PF00233; PDEase; 1.
DR PRINTS; PR00387; PDIESTERASE1.
DR SMART; SM00471; HDc; 1.
DR PROSITE; PS00126; PDEASE_I; 1.
KW Hydrolase.
SQ SEQUENCE 459 AA; 52680 MW; A3F26E95C7FC00A5 CRC64;

Query Match 61.4%; Score 1377.5; DB 11; Length 459;
Best Local Similarity 63.2%; Pred. No. 1.1e-115;
Matches 254; Conservative 63; Mismatches 80; Indels 5; Gaps 2;

```
Qy         11 GDVRVRSRAGFESERRGSHPYIDFRIFHSQSEIEVSVSARNIRRLLSFQRYLRSSRFFRG 70
Db         41 GDVRLRGQTGVPAERRGSYPFIDFRLLNNTTHSGEIGSKKKVRRLLSFQRHFHESRLLRG 100

Qy         71 TAVSNSLNILDDDYNGQAKCMLEKVGNWNFDIFLFDRLTNGNSLVSLTFHLFSLHGLIEY 130
Db        101 MTPQAPLHLLDEDYLGQARHMLSKVGMWDFDIFLFDRLTNGNSLVTLLCHLFNSHGLIHH 160

Qy        131 FHLDMMKLRRFLVMIQEDYHSQNPYHNAVHAADVTQAMHCYLKEPKLANSVTPWDILLSL 190
Db        161 FKLDMVTLHRFLVMVQEDYHGHNPYHNAVHAADVTQAMHCYLKEPKLASFLTPLDIMLGL 220

Qy        191 IAAATHDLDHPGVNQPFLIKTNHYLATLYKNTSVLENHHWRSAVGLLRESGLFSHLPLES 250
Db        221 LAAAAHDVDHPGVNQPFLIKTNHHLANLYQNMSVLENHHWRSTIGMLRESRLLAHLPKEM 280

Qy        251 RQQMETQIGALILATDISRQNEYLSLFRSHLDRGDLCLEDTRHRHLVLQMALKCADICNP 310
Db        281 TQDIEQQLGSLILATDINRQNEFLTRLKAHLHNKDLRLENIQDRHFMLQIALKCADICNP 340

Qy        311 CRTWELSKQWSEKVTEEFFHQGDIEKKYHLGVSPLCDRHTESIANIQIGFMTYLVEPLFT 370
Db        341 CRIWEMSKQWSERVCEEFYRQGDLEQKFELEISPLCNQQKDSIPSIQIGFMTYIVEPLFR 400

Qy        371 EWARFS-NTRLSQTMLGHVGLNKASWKGL----QREQSSSED 407
Db        401 EWARFTGNSTLSESMLNHLAHNKAQWKSLLSNQHRRRGSGQD 442
```

RESULT 6
Q8VIE3
ID Q8VIE3 PRELIMINARY; PRT; 359 AA.
AC Q8VIE3;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)

```
DE   Cyclic nucleotide phosphodiesterase 7B3 (EC 3.1.4.17).
GN   RNPDE7B.
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Testis;
RA   Sasaki T., Kotera J., Omori K.;
RT   "Novel alternative splice variants of rat PDE7B.";
RL   Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AB057410; BAB79638.1; -.
DR   GO; GO:0004114; F:3',5'-cyclic-nucleotide phosphodiesterase a. . .; IEA.
DR   GO; GO:0016787; F:hydrolase activity; IEA.
DR   GO; GO:0007165; P:signal transduction; IEA.
DR   InterPro; IPR003607; Met_phsphohydro.
DR   InterPro; IPR002073; PDEase.
DR   Pfam; PF00233; PDEase; 1.
DR   PRINTS; PR00387; PDIESTERASE1.
DR   SMART; SM00471; HDc; 1.
DR   PROSITE; PS00126; PDEASE_I; 1.
KW   Hydrolase.
SQ   SEQUENCE   359 AA;  41456 MW;  0FF72792737CE48A CRC64;

  Query Match             54.9%;  Score 1231.5;  DB 11;  Length 359;
  Best Local Similarity   67.0%;  Pred. No. 1.2e-102;
  Matches  225;  Conservative   51;  Mismatches   55;  Indels    5;  Gaps    2;

Qy         77 LNILDDDYNGQAKCMLEKVGNWNFDIFLFDRLTNGNSLVSLTFHLFSLHGLIEYFHLDMM 136
              |::||:|| |||: || ||| |:||||||||||||||||:|  |||: |||| :| |||:
Db          7 LHLLDEDYLGQARHMLSKVGMWDFDIFLFDRLTNGNSLVTLLCHLFNSHGLIHHFKLDMV 66

Qy        137 KLRRFLVMIQEDYHSQNPYHNAVHAADVTQAMHCYLKEPKLANSVTPWDILLSLIAAATH 196
              | |||||:|||||  ||||||||||||||||||||||||: :|| ||:| |:||| |
Db         67 TLHRFLVMVQEDYHGHNPYHNAVHAADVTQAMHCYLKEPKLASFLTPLDIMLGLLAAAAH 126

Qy        197 DLDHPGVNQPFLIKTNHYLATLYKNTSVLENHHWRSAVGLLRESGLFSHLPLESRQQMET 256
              |:|||||||||||||:|| ||:| |||||||||| :|:|||| | :||| |  | :|
Db        127 DVDHPGVNQPFLIKTNHHLANLYQNMSVLENHHWRSTIGMLRESRLLAHLPKEMTQDIEQ 186

Qy        257 QIGALILATDISRQNEYLSLFRSHLDRGDLCLEDTRHRHLVLQMALKCADICNPCRTWEL 316
              |:|:|||||||:||||:|:  ::||   || ||: : || :||:||||||||||| ||:
Db        187 QLGSLILATDINRQNEFLTRLKAHLHNKDLRLENIQDRHFMLQIALKCADICNPCRIWEM 246

Qy        317 SKQWSEKVTEEFFHQGDIEKKYHLGVSPLCDRHTESIANIQIGFMTYLVEPLFTEWARFS 376
              ||||||:| |||: |||:|:|: | :||||::  :|| :|||||||:||||| |||||:
Db        247 SKQWSERVCEEFYRQGDLEQKFELEISPLCNQQKDSIPSIQIGFMTYIVEPLFREWARFT 306

Qy        377 -NTRLSQTMLGHVGLNKASWKGL----QREQSSSED 407
               |: ||::|| |:  ||| || |     | : | :|
Db        307 GNSTLSESMLNHLAHNKAQWKSLLSNQHRRRGSGQD 342


RESULT 7
Q86V65
ID   Q86V65      PRELIMINARY;      PRT;   162 AA.
AC   Q86V65;
DT   01-JUN-2003 (TrEMBLrel. 24, Created)
DT   01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Phosphodiesterase isozyme 7 (Fragment).
GN   PDE7.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=99320215; PubMed=10393044;
RA   Zhou L., Thompson W.J., Potter D.E.;
RT   "Multiple cyclic nucleotide phosphodiesterases in human trabecular
RT   meshwork cells.";
RL   Invest. Ophthalmol. Vis. Sci. 40:1745-1752(1999).
RN   [2]
RP   SEQUENCE FROM N.A.
RA   Zhou L., Thompson W.J., Potter D.E.;
RL   Submitted (APR-2003) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AY266364; AAP31236.1; -.
DR   GO; GO:0004114; F:3',5'-cyclic-nucleotide phosphodiesterase a. . .; IEA.
DR   GO; GO:0007165; P:signal transduction; IEA.
DR   InterPro; IPR002073; PDEase.
FT   NON_TER       1      1
FT   NON_TER     162    162
SQ   SEQUENCE   162 AA;  18867 MW;  E7D548571291EEDA CRC64;

  Query Match             32.0%;  Score 717;  DB 4;  Length 162;
  Best Local Similarity   100.0%;  Pred. No. 1.1e-56;
  Matches  139;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 DQTALYIRMLGDVRVRSRAGFESERRGSHPYIDFRIFHSQSEIEVSVSARNIRRLLSFQR 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         24 DQTALYIRMLGDVRVRSRAGFESERRGSHPYIDFRIFHSQSEIEVSVSARNIRRLLSFQR 83

Qy         61 YLRSSRFFRGTAVSNSLNILDDDYNGQAKCMLEKVGNWNFDIFLFDRLTNGNSLVSLTFH 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         84 YLRSSRFFRGTAVSNSLNILDDDYNGQAKCMLEKVGNWNFDIFLFDRLTNGNSLVSLTFH 143

Qy        121 LFSLHGLIEYFHLDMMKLR 139
              |||||||||||||||||||
Db        144 LFSLHGLIEYFHLDMMKLR 162


RESULT 8
Q9EQR7
ID   Q9EQR7      PRELIMINARY;      PRT;   771 AA.
AC   Q9EQR7;
DT   01-MAR-2001 (TrEMBLrel. 16, Created)
DT   01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Cyclic AMP phosphodiesterase PDE4A10 (Fragment).
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Rena G., Begg F., Ross A., MacKenzie C., McPhee I., Campbell L.,
RA   Huston E., Sullivan M., Houslay M.D.;
RT   "Molecular cloning, genomic positioning, promoter identification and
RT   characterisation of the novel cAMP-specific phosphodiesterase,
RT   PDE4A10.";
RL   Mol. Pharmacol. 0:0-0(2001).
DR   EMBL; AF110461; AAF14352.2; -.
DR   GO; GO:0004114; F:3',5'-cyclic-nucleotide phosphodiesterase a. . .; IEA.
DR   GO; GO:0003824; F:catalytic activity; IEA.
DR   GO; GO:0007165; P:signal transduction; IEA.
DR   InterPro; IPR003607; Met_phsphohydro.
DR   InterPro; IPR002073; PDEase.
DR   Pfam; PF00233; PDEase; 1.
DR   PRINTS; PR00387; PDIESTERASE1.
DR   SMART; SM00471; HDc; 1.
DR   PROSITE; PS00126; PDEASE_I; 1.
FT   NON_TER       1      1
FT   NON_TER     771    771
SQ   SEQUENCE   771 AA;  85459 MW;  D20712E515CDAF0B CRC64;

  Query Match             24.7%;  Score 555;  DB 11;  Length 771;
  Best Local Similarity   32.6%;  Pred. No. 4.2e-41;
  Matches  127;  Conservative   77;  Mismatches  154;  Indels   32;  Gaps    7;

Qy          8 RMLGDVRVRSRAGFESERRGSHPYIDFRIFHSQSEIEVSVSARNIRRLLSFQR----YLR 63
              | |  :   ||:| :     |: ::|      |:|:|:       |   :||:     ||
Db        190 RELTHLSEMSRSGNQVSEYISNTFLD-----KQNEVEIPSPTPRQR---AFQQPPPSVLR 241

Qy         64 SSR------FFRGTAVSNSLNI------LDDDYNGQAKCMLEKVGNWNFDIFLFDRLTNG 111
```

```
Db        242 QSQPMSQITGLKKLVHTGSLNTNVPRFGVKTDQEDLLAQELENLSKWGLNIFCVSEYAGG 301

Qy        112 NSLVSLTFHLFSLHGLIEYFHLDMMKLRRFLVMIQEDYHSQNPYHNAVHAADVTQAMHCY 171

Db        302 RSLSCIMYTIFQERDLLKKFHIPVDTMMMYMLTLEDHYHADVAYHNSLHAADVLQSTHVL 361

Qy        172 LKEPKLANSVTPWDILLSLIAAATHDLDHPGVNQPFLIKTNHYLATLYKNTSVLENHHWR 231

Db        362 LATPALDAVFTDLEILAALFAAAIHDVDHPGVSNQFLINTNSELALMYNDESVLENHHLA 421

Qy        232 SAVGLLRESG--LFSHLPLESRQQMETQIGALILATDISRQNEYLSLFRSHLD------R 283

Db        422 VGFKLLQEENCDIFQNLSKRQRQSLRKMVIDMVLATDMSKHMTLLADLKTMVETKKVTSS 481

Qy        284 GDLCLEDTRHRHLVLQMALKCADICNPCRTWELSKQWSEKVTEEFFHQGDIEKKYHLGVS 343

Db        482 GVLLLDNYSDRIQVLRNMVHCADLSNPTKPLELYRQWTDRIMAEFFQQGDRERERGMEIS 541

Qy        344 PLCDRHTESIANIQIGFMTYLVEPLFTEWA 373

Db        542 PMCDKHTASVEKSQVGFIDYIVHPLWETWA 571
```

RESULT 9
Q9QXI7
ID Q9QXI7 PRELIMINARY; PRT; 721 AA.
AC Q9QXI7;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE cAMP-specific phosphodiesterase (Phosphodiesterase 4B, cAMP
DE specific).
GN PDE4B.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=SWISS WEBSTER;
RA Cherry J.A., Thompson B.E., Pho V.;
RT "Cloning and biochemical characterization of cyclic AMP
RT phosphodiesterase isoforms in the mouse.";
RL Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=SWISS WEBSTER;
RA Cherry J.A., Thompson B.E., Pho V.;
RT "Diazepam and rolipram differentially inhibit cAMP-specific
RT phosphodiesterases PDE4A1 and PDE4B3 in the mouse.";
RL Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AF208023; AAF19202.2; -.
DR EMBL; AJ297397; CAB96770.1; -.
DR MGD; MGI:99557; Pde4b.
DR GO; GO:0004114; F:3',5'-cyclic-nucleotide phosphodiesterase a. . .; IEA.
DR GO; GO:0003824; F:catalytic activity; IEA.
DR GO; GO:0007165; P:signal transduction; IEA.
DR InterPro; IPR003607; Met_phsphohydro.
DR InterPro; IPR002073; PDEase.
DR Pfam; PF00233; PDEase; 1.
DR PRINTS; PR00387; PDIESTERASE1.
DR SMART; SM00471; HDc; 1.
DR PROSITE; PS00126; PDEASE_I; 1.
SQ SEQUENCE 721 AA; 82074 MW; 302311CA44636E7F CRC64;

Query Match 24.6%; Score 551; DB 11; Length 721;
Best Local Similarity 31.8%; Pred. No. 8.7e-41;
Matches 122; Conservative 84; Mismatches 152; Indels 26; Gaps 6;

```
Qy          8 RMLGDVRVRSRAGFESERRGSHPYIDFRIFHSQSEIEVSVSARNIRR---------LLSF 58

Db        241 RELTHLSEMSRSGNQVSEYISNTFLD-----KQNDVEIPSPTQKDREKKKKQQLMTQISG 295

Qy         59 QRYLRSSRFFRGTAVSN-SLNILDDDYNGQAKCMLEKVGNWNFDIFLFDRLTNGNSLVSL 117

Db        296 VKKLMHSSSLNNTSISRFGINTENEDHLAKE---LEDLNKWGLNIFNVAGYSHNRPLTCI 352

Qy        118 TFHLFSLHGLIEYFHLDMMKLRRFLVMIQEDYHSQNPYHNAVHAADVTQAMHCYLKEPKL 177

Db        353 MYAIFQERDLLKTFKISSDTFVTYMMTLEDHYHSDVAYHNSLHAADVAQSTHVLLSTPAL 412

Qy        178 ANSVTPWDILLSLIAAATHDLDHPGVNQPFLIKTNHYLATLYKNTSVLENHHWRSAVGLL 237

Db        413 DAVFTDLEILAAIFAAAIHDVDHPGVSNQFLINTNSELALMYNDESVLENHHLAVGFKLL 472

Qy        238 RES--GLFSHLPLESRQQMETQIGALILATDISRQNEYLSLFRSHLD------RGDLCLE 289

Db        473 QEEHCDIFQNLTKKQRQTLRKMVIDMVLATDMSKHMSLLADLKTMVETKKVTSSGVLLLD 532

Qy        290 DTRHRHLVLQMALKCADICNPCRTWELSKQWSEKVTEEFFHQGDIEKKYHLGVSPLCDRH 349

Db        533 NYTDRIQVLRNMVHCADLSNPTKSLELYRQWTDRIMEEFFQQGDKERERGMEISPMCDKH 592

Qy        350 TESIANIQIGFMTYLVEPLFTEWA 373

Db        593 TASVEKSQVGFIDYIVHPLWETWA 616
```

RESULT 10
Q91VY2
ID Q91VY2 PRELIMINARY; PRT; 542 AA.
AC Q91VY2;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Similar to phosphodiesterase 4B, cAMP-specific (Dunce (Drosophila)-
DE homolog phosphodiesterase E4) (Fragment).
GN PDE4B OR EDNRA.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Breast tumor;
RA Strausberg R.;
RL Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
DR EMBL; BC007155; AAH07155.1; -.
DR MGD; MGI:105923; Ednra.
DR MGD; MGI:99557; Pde4b.
DR GO; GO:0004114; F:3',5'-cyclic-nucleotide phosphodiesterase a. . .; IEA.
DR GO; GO:0003824; F:catalytic activity; IEA.
DR GO; GO:0007165; P:signal transduction; IEA.
DR InterPro; IPR003607; Met_phsphohydro.
DR InterPro; IPR002073; PDEase.
DR Pfam; PF00233; PDEase; 1.
DR PRINTS; PR00387; PDIESTERASE1.
DR SMART; SM00471; HDc; 1.
DR PROSITE; PS00126; PDEASE_I; 1.
FT NON_TER 1 1
SQ SEQUENCE 542 AA; 62279 MW; 8B6296D416275B34 CRC64;

Query Match 24.5%; Score 550; DB 11; Length 542;
Best Local Similarity 31.8%; Pred. No. 7.2e-41;
Matches 122; Conservative 84; Mismatches 152; Indels 26; Gaps 6;

```
Qy          8 RMLGDVRVRSRAGFESERRGSHPYIDFRIFHSQSEIEVSVSARNIRR---------LLSF 58

Db         62 RELTHLSEMSRSGNQVSEYISNTFLD-----KQNDVEIPSPTQKDREKKKKQQLMTQISG 116

Qy         59 QRYLRSSRFFRGTAVSN-SLNILDDDYNGQAKCMLEKVGNWNFDIFLFDRLTNGNSLVSL 117

Db        117 VKKLMHSSSLNNTSISRFGVNTENEDHLAKE---LEDLNKWGLNIFNVAGYSHNRPLTCI 173

Qy        118 TFHLFSLHGLIEYFHLDMMKLRRFLVMIQEDYHSQNPYHNAVHAADVTQAMHCYLKEPKL 177
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Db        174 MYAIFQERDLLKTFKISSDTFVTYMMTLEDHYHSDVAYHNSLHAADVAQSTHVLLSTPAL 233

Qy        178 ANSVTPWDILLSLIAAATHDLDHPGVNQPFLIKTNHYLATLYKNTSVLENHHWRSAVGLL 237

Db        234 DAVFTDLEILAAIFAAAIHDVDHPGVSNQFLINTNSELALMYNDESVLENHHLAVGFKLL 293

Qy        238 RES--GLFSHLPLESRQQMETQIGALILATDISRQNEYLSLFRSHLD------RGDLCLE 289

Db        294 QEEHCDIFQNLTKKQRQTLRKMVIDMVLATDMSKHMSLLADLKTMVETKKVTSSGVLLLD 353

Qy        290 DTRHRHLVLQMALKCADICNPCRTWELSKQWSEKVTEEFFHQGDIEKKYHLGVSPLCDRH 349

Db        354 NYTDRIQVLRNMVHCADLSNPTKSLELYRQWTDRIMEEFFQQGDKERERGMEISPMCDKH 413

Qy        350 TESIANIQIGFMTYLVEPLFTEWA 373

Db        414 TASVEKSQVGFIDYIVHPLWETWA 437
```

RESULT 11
Q13945
ID Q13945 PRELIMINARY; PRT; 606 AA.
AC Q13945;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE 3',5'-cyclic AMP phosphodiesterase (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93314968; PubMed=8392015;
RA Obernolte R., Bhakta S., Alvarez R., Bach C., Mulkins M., Jarnagin K.,
RA Shelton E.R.;
RT "The cDNA of a human lymphocyte cyclic-AMP phosphodiesterase (PDE IV)
RT reveals a multigene family.";
RL Gene 129:239-247(1993).
DR EMBL; L12686; AAA35643.1; -.
DR PIR; JC1519; JC1519.
DR GO; GO:0004114; F:3',5'-cyclic-nucleotide phosphodiesterase a. . .; IEA.
DR GO; GO:0003824; F:catalytic activity; IEA.
DR GO; GO:0007165; P:signal transduction; IEA.
DR InterPro; IPR003607; Met_phsphohydro.
DR InterPro; IPR002073; PDEase.
DR Pfam; PF00233; PDEase; 1.
DR PRINTS; PR00387; PDIESTERASE1.
DR SMART; SM00471; HDc; 1.
DR PROSITE; PS00126; PDEASE_I; 1.
KW cAMP.
FT NON_TER 1 1
SQ SEQUENCE 606 AA; 68663 MW; 256BD63B32C79398 CRC64;

Query Match 24.5%; Score 550; DB 4; Length 606;
Best Local Similarity 31.8%; Pred. No. 8.5e-41;
Matches 122; Conservative 84; Mismatches 152; Indels 26; Gaps 6;

```
Qy          8 RMLGDVRVRSRAGFESERRGSHPYIDFRIFHSQSEIEVSVSARNIRR---------LLSF 58

Db        126 RELTHLSEMSRSGNQVSEYISNTFLD-----KQNDVEIPSPTQKDREKKKKQQLMTQISG 180

Qy         59 QRYLRSSRFFRGTAVSN-SLNILDDDYNGQAKCMLEKVGNWNFDIFLFDRLTNGNSLVSL 117

Db        181 VKKLMHSSSLNNTSISRFGVNTENEDHLAKE---LEDLNKWGLNIFNVAGYSHNRPLTCI 237

Qy        118 TFHLFSLHGLIEYFHLDMMKLRRFLVMIQEDYHSQNPYHNAVHAADVTQAMHCYLKEPKL 177

Db        238 MYAIFQERDLLKTFRISSDTFITYMMTLEDHYHSDVAYHNSLHAADVAQSTHVLLSTPAL 297

Qy        178 ANSVTPWDILLSLIAAATHDLDHPGVNQPFLIKTNHYLATLYKNTSVLENHHWRSAVGLL 237

Db        298 DAVFTDLEILAAIFAAAIHDVDHPGVSNQFLINTNSELALMYNDESVLENHHLAVGFKLL 357

Qy        238 RES--GLFSHLPLESRQQMETQIGALILATDISRQNEYLSLFRSHLD------RGDLCLE 289

Db        358 QEEHCDIFMNLTKKQRQTLRKMVIDMVLATDMSKHMSLLADLKTMVETKKVTSSGVLLLD 417

Qy        290 DTRHRHLVLQMALKCADICNPCRTWELSKQWSEKVTEEFFHQGDIEKKYHLGVSPLCDRH 349

Db        418 NYTDRIQVLRNMVHCADLSNPTKSLELYRQWTDRIMEEFFQQGDKERERGMEISPMCDKH 477

Qy        350 TESIANIQIGFMTYLVEPLFTEWA 373

Db        478 TASVEKSQVGFIDYIVHPLWETWA 501
```

RESULT 12
Q8VD81
ID Q8VD81 PRELIMINARY; PRT; 659 AA.
AC Q8VD81;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE cAMP-specific phosphodiesterase isoform PDE4B4.
GN PDE4B.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Sprague-Dawley; TISSUE=Brain cortex;
RA Olsen A.E., Bolger G.B.;
RT "Novel PDE4B cAMP-specific phosphodiesterase isoforms and related
RT technology.";
RL Submitted (NOV-1999) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AF202733; AAL31764.1; -.
DR GO; GO:0004114; F:3',5'-cyclic-nucleotide phosphodiesterase a. . .; IEA.
DR GO; GO:0003824; F:catalytic activity; IEA.
DR GO; GO:0007165; P:signal transduction; IEA.
DR InterPro; IPR003607; Met_phsphohydro.
DR InterPro; IPR002073; PDEase.
DR Pfam; PF00233; PDEase; 1.
DR PRINTS; PR00387; PDIESTERASE1.
DR SMART; SM00471; HDc; 1.
DR PROSITE; PS00126; PDEASE_I; 1.
SQ SEQUENCE 659 AA; 75059 MW; 500099D1E38E0882 CRC64;

Query Match 24.5%; Score 550; DB 11; Length 659;
Best Local Similarity 31.8%; Pred. No. 9.5e-41;
Matches 122; Conservative 84; Mismatches 152; Indels 26; Gaps 6;

```
Qy          8 RMLGDVRVRSRAGFESERRGSHPYIDFRIFHSQSEIEVSVSARNIRR---------LLSF 58

Db        179 RELTHLSEMSRSGNQVSEYISNTFLD-----KQNDVEIPSPTQKDREKKKKQQLMTQISG 233

Qy         59 QRYLRSSRFFRGTAVSN-SLNILDDDYNGQAKCMLEKVGNWNFDIFLFDRLTNGNSLVSL 117

Db        234 VKKLMHSSSLNNTSISRFGVNTENEDHLAKE---LEDLNKWGLNIFNVAGYSHNRPLTCI 290

Qy        118 TFHLFSLHGLIEYFHLDMMKLRRFLVMIQEDYHSQNPYHNAVHAADVTQAMHCYLKEPKL 177

Db        291 MYAIFQERDLLKTFKISSDTFVTYMMTLEDHYHSDVAYHNSLHAADVAQSTHVLLSTPAL 350

Qy        178 ANSVTPWDILLSLIAAATHDLDHPGVNQPFLIKTNHYLATLYKNTSVLENHHWRSAVGLL 237

Db        351 DAVFTDLEILAAIFAAAIHDVDHPGVSNQFLINTNSELALMYNDESVLENHHLAVGFKLL 410

Qy        238 RES--GLFSHLPLESRQQMETQIGALILATDISRQNEYLSLFRSHLD------RGDLCLE 289

Db        411 QEEHCDIFQNLTKKQRQTLRKMVIDMVLATDMSKHMSLLADLKTMVETKKVTSSGVLLLD 470

Qy        290 DTRHRHLVLQMALKCADICNPCRTWELSKQWSEKVTEEFFHQGDIEKKYHLGVSPLCDRH 349
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Db        471 NYTDRIQVLRNMVHCADLSNPTKSLELYRQWTDRIMEEFFQQGDKERERGMEISPMCDKH 530

Qy        350 TESIANIQIGFMTYLVEPLFTEWA 373
              | |:   |:||: |:| ||:  ||
Db        531 TASVEKSQVGFIDYIVHPLWETWA 554


RESULT 13
Q8VBU5
ID   Q8VBU5      PRELIMINARY;      PRT;   721 AA.
AC   Q8VBU5;
DT   01-MAR-2002 (TrEMBLrel. 20, Created)
DT   01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Phosphodiesterase 4B.
GN   PDE4B.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=DBA/2J, and C57BL/6J; TISSUE=Brain;
RA   Fehr C., Belknap J.K., Crabbe J.C., Buck K.J.;
RT   "High resolution mapping of a quantitative trait locus for acute
RT   ethanol withdrawal on mouse chromosome 4 and characterization of
RT   potential candidate genes.";
RL   Submitted (DEC-2000) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF326556; AAL37402.1; -.
DR   EMBL; AF326555; AAL37401.1; -.
DR   MGD; MGI:99557; Pde4b.
DR   GO; GO:0004114; F:3',5'-cyclic-nucleotide phosphodiesterase a. . .; IEA.
DR   GO; GO:0003824; F:catalytic activity; IEA.
DR   GO; GO:0007165; P:signal transduction; IEA.
DR   InterPro; IPR003607; Met_phsphohydro.
DR   InterPro; IPR002073; PDEase.
DR   Pfam; PF00233; PDEase; 1.
DR   PRINTS; PR00387; PDIESTERASE1.
DR   SMART; SM00471; HDc; 1.
DR   PROSITE; PS00126; PDEASE_I; 1.
SQ   SEQUENCE   721 AA;  82075 MW;  B3725A478A7612FB CRC64;

  Query Match             24.5%;  Score 550;  DB 11;  Length 721;
  Best Local Similarity   31.8%;  Pred. No. 1.1e-40;
  Matches  122;  Conservative   84;  Mismatches  152;  Indels   26;  Gaps    6;

Qy          8 RMLGDVRVRSRAGFESERRGSHPYIDFRIFHSQSEIEVSVSARNIRR---------LLSF 58
              | |  :   ||:| :     |: ::|      |:::|:   :  |           :|
Db        241 RELTHLSEMSRSGNQVSEYISNTFLD-----KQNDVEIPSPTQKDREKKKKQQLMTQISG 295

Qy         59 QRYLRSSRFFRGTAVSN-SLNILDDDYNGQAKCMLEKVGNWNFDIFLFDRLTNGNSLVSL 117
               :  |  |      |::|   :|  ::|:  :    || :  |  :||     ::   |  :
Db        296 VKKLMHSSSLNNTSISRFGVNTENEDHLAKE---LEDLNKWGLNIFNVAGYSHNRPLTCI 352

Qy        118 TFHLFSLHGLIEYFHLDMMKLRRFLVMIQEDYHSQNPYHNAVHAADVTQAMHCYLKEPKL 177
               : :|    |:: | :       ::: ::: |||   |||::|||| |: |  |  | |
Db        353 MYAIFQERDLLKTFKISSDTFVTYMMTLEDHYHSDVAYHNSLHAADVAQSTHVLLSTPAL 412

Qy        178 ANSVTPWDILLSLIAAATHDLDHPGVNQPFLIKTNHYLATLYKNTSVLENHHWRSAVGLL 237
                 |  :|| :: ||| ||:|||||:  ||| ||  || :| : |||||||        ||
Db        413 DAVFTDLEILAAIFAAAIHDVDHPGVSNQFLINTNSELALMYNDESVLENHHLAVGFKLL 472

Qy        238 RES--GLFSHLPLESRQQMETQIGALILATDISRQNEYLSLFRSHLD------RGDLCLE 289
              :|    :| :|  : || :   :  ::||||:|:    |:  :: ::       | | |:
Db        473 QEEHCDIFQNLTKKQRQTLRKMVIDMVLATDMSKHMSLLADLKTMVETKKVTSSGVLLLD 532

Qy        290 DTRHRHLVLQMALKCADICNPCRTWELSKQWSEKVTEEFFHQGDIEKKYHLGVSPLCDRH 349
              :   |  ||:  : |||: || :: || :||:::: |||| ||| |::  : :||:||:|
Db        533 NYTDRIQVLRNMVHCADLSNPTKSLELYRQWTDRIMEEFFQQGDKERERGMEISPMCDKH 592

Qy        350 TESIANIQIGFMTYLVEPLFTEWA 373
              | |:   |:||: |:| ||:  ||
Db        593 TASVEKSQVGFIDYIVHPLWETWA 616


RESULT 14
Q8VD82
ID   Q8VD82      PRELIMINARY;      PRT;   736 AA.
AC   Q8VD82;
DT   01-MAR-2002 (TrEMBLrel. 20, Created)
DT   01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   cAMP-specific phosphodiesterase isoform PDE4B1.
GN   PDE4B.
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=Sprague-Dawley; TISSUE=Brain cortex;
RA   Olsen A.E., Bolger G.B.;
RT   "Novel PDE4B cAMP-specific phosphodiesterase isoforms and related
RT   technology.";
RL   Submitted (NOV-1999) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF202732; AAL31763.1; -.
DR   GO; GO:0004114; F:3',5'-cyclic-nucleotide phosphodiesterase a. . .; IEA.
DR   GO; GO:0003824; F:catalytic activity; IEA.
DR   GO; GO:0007165; P:signal transduction; IEA.
DR   InterPro; IPR003607; Met_phsphohydro.
DR   InterPro; IPR002073; PDEase.
DR   Pfam; PF00233; PDEase; 1.
DR   PRINTS; PR00387; PDIESTERASE1.
DR   SMART; SM00471; HDc; 1.
DR   PROSITE; PS00126; PDEASE_I; 1.
SQ   SEQUENCE   736 AA;  83348 MW;  E78509269A8DF169 CRC64;

  Query Match             24.5%;  Score 550;  DB 11;  Length 736;
  Best Local Similarity   31.8%;  Pred. No. 1.1e-40;
  Matches  122;  Conservative   84;  Mismatches  152;  Indels   26;  Gaps    6;

Qy          8 RMLGDVRVRSRAGFESERRGSHPYIDFRIFHSQSEIEVSVSARNIRR---------LLSF 58
              | |  :   ||:| :     |: ::|      |:::|:   :  |           :|
Db        256 RELTHLSEMSRSGNQVSEYISNTFLD-----KQNDVEIPSPTQKDREKKKKQQLMTQISG 310

Qy         59 QRYLRSSRFFRGTAVSN-SLNILDDDYNGQAKCMLEKVGNWNFDIFLFDRLTNGNSLVSL 117
               :  |  |      |::|   :|  ::|:  :    || :  |  :||     ::   |  :
Db        311 VKKLMHSSSLNNTSISRFGVNTENEDHLAKE---LEDLNKWGLNIFNVAGYSHNRPLTCI 367

Qy        118 TFHLFSLHGLIEYFHLDMMKLRRFLVMIQEDYHSQNPYHNAVHAADVTQAMHCYLKEPKL 177
               : :|    |:: | :       ::: ::: |||   |||::|||| |: |  |  | |
Db        368 MYAIFQERDLLKTFKISSDTFVTYMMTLEDHYHSDVAYHNSLHAADVAQSTHVLLSTPAL 427

Qy        178 ANSVTPWDILLSLIAAATHDLDHPGVNQPFLIKTNHYLATLYKNTSVLENHHWRSAVGLL 237
                 |  :|| :: ||| ||:|||||:  ||| ||  || :| : |||||||        ||
Db        428 DAVFTDLEILAAIFAAAIHDVDHPGVSNQFLINTNSELALMYNDESVLENHHLAVGFKLL 487

Qy        238 RES--GLFSHLPLESRQQMETQIGALILATDISRQNEYLSLFRSHLD------RGDLCLE 289
              :|    :| :|  : || :   :  ::||||:|:    |:  :: ::       | | |:
Db        488 QEEHCDIFQNLTKKQRQTLRKMVIDMVLATDMSKHMSLLADLKTMVETKKVTSSGVLLLD 547

Qy        290 DTRHRHLVLQMALKCADICNPCRTWELSKQWSEKVTEEFFHQGDIEKKYHLGVSPLCDRH 349
              :   |  ||:  : |||: || :: || :||:::: |||| ||| |::  : :||:||:|
Db        548 NYTDRIQVLRNMVHCADLSNPTKSLELYRQWTDRIMEEFFQQGDKERERGMEISPMCDKH 607

Qy        350 TESIANIQIGFMTYLVEPLFTEWA 373
              | |:   |:||: |:| ||:  ||
Db        608 TASVEKSQVGFIDYIVHPLWETWA 631


RESULT 15
Q8IV84
ID   Q8IV84      PRELIMINARY;      PRT;   687 AA.
AC   Q8IV84;
DT   01-MAR-2003 (TrEMBLrel. 23, Created)
DT   01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
```

```
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   cAMP-specific phosphodiesterase PDE4D8.
GN   PDE4D.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Wang D., Bugaj-Gaweda B., Kwan M., Unterbeck A., De Vivo M.;
RL   Submitted (AUG-2002) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF536977; AAN10119.1; -.
DR   GO; GO:0004114; F:3',5'-cyclic-nucleotide phosphodiesterase a. . .; IEA.
DR   GO; GO:0007165; P:signal transduction; IEA.
DR   InterPro; IPR002073; PDEase.
DR   Pfam; PF00233; PDEase; 1.
DR   PRINTS; PR00387; PDIESTERASE1.
DR   PROSITE; PS00126; PDEASE_I; 1.
SQ   SEQUENCE   687 AA;  77646 MW;  91137D110DC3477C CRC64;

  Query Match             24.4%;  Score 548;  DB 4;  Length 687;
  Best Local Similarity   31.9%;  Pred. No. 1.5e-40;
  Matches  123;  Conservative   82;  Mismatches  149;  Indels   32;  Gaps    7;

Qy          8 RMLGDVRVRSRAGFESERRGSHPYIDFRIFHSQSEIEV--------SVSARNIRRLLSFQ 59
              | |  :   ||:| :      |: ::|      | |:|:            | : ::   :
Db        192 RELTHLSEMSRSGNQVSEFISNTFLD-----KQHEVEIPSPTQKEKEKKKRPMSQISGVK 246

Qy         60 RYLRSSRFFRGTAVSNS----LNILDDDYNGQAKCMLEKVGNWNFDIFLFDRLTNGNSLV 115
             : : ||      :::||      :  :  :  ||  || |  |   :|    |:     |
Db        247 KLMHSS------SLTNSSIPRFGVKTEQEDVLAK-ELEDVNKWGLHVFRIAELSGNRPLT 299

Qy        116 SLTFHLFSLHGLIEYFHLDMMKLRRFLVMIQEDYHSQNPYHNAVHAADVTQAMHCYLKEP 175
              :   :|    |:: | : :  |  :|: ::: ||:   ||| :||||| |: |  |  |
Db        300 VIMHTIFQERDLLKTFKIPVDTLITYLMTLEDHYHADVAYHNNIHAADVVQSTHVLLSTP 359

Qy        176 KLANSVTPWDILLSLIAAATHDLDHPGVNQPFLIKTNHYLATLYKNTSVLENHHWRSAVG 235
              |    |  :|| :: |:| ||:||||||:  ||| ||  || :| ::|||||||
Db        360 ALEAVFTDLEILAAIFASAIHDVDHPGVSNQFLINTNSELALMYNDSSVLENHHLAVGFK 419

Qy        236 LLRES--GLFSHLPLESRQQMETQIGALILATDISRQNEYLSLFRSHLD------RGDLC 287
             ||:|   |:| :|  : || :   :  ::||||:|:    |:  :: ::       | |
Db        420 LLQEENCGIFQNLTKKQRQSLRKMVIDIVLATDMSKHMNLLADLKTMVETKKVTSSGVLL 479

Qy        288 LEDTRHRHLVLQMALKCADICNPCRTWELSKQWSEKVTEEFFHQGDIEKKYHLGVSPLCD 347
             |::   |  |||  : |||: || :  :| :||:::: |||| ||| |::  : :||:||
Db        480 LDNYSDRIQVLQNMVHCADLSNPTKPLQLYRQWTDRIMEEFFRQGDRERERGMEISPMCD 539

Qy        348 RHTESIANIQIGFMTYLVEPLFTEWA 373
              :|  |:   |:||: |:| ||:  ||
Db        540 KHNASVEKSQVGFIDYIVHPLWETWA 565


Search completed: May 26, 2004, 09:26:36
Job time : 48 secs
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GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: May 26, 2004, 09:24:28 ; Search time 97 Seconds
(without alignments)
1240.879 Million cell updates/sec

Title: US-09-966-781A-1
Perfect score: 2243
Sequence: 1 DQTALYIRMLGDVRVRSRAG.....DTDAAFELNSQLLPQENRLS 426

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_29Jan04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	2243	100.0	426	5	AAE24527	Aae24527 Human PDE
2	2243	100.0	446	5	AAE24532	Aae24532 Human PDE
3	2243	100.0	482	5	AAE24531	Aae24531 Human PDE
4	2243	100.0	498	2	AAW00094	Aaw00094 cAMP phos
5	2243	100.0	498	2	AAY49808	Aay49808 Human gli
6	2243	100.0	498	3	AAB20619	Aab20619 pTM22 hum
7	2116	94.3	426	5	AAE24529	Aae24529 Rat PDE7
8	2116	94.3	428	5	AAE24533	Aae24533 Rat PDE7a
9	2105	93.8	426	5	AAE24528	Aae24528 Mouse PDE
10	2105	93.8	456	5	AAE24530	Aae24530 Mouse PDE
11	1910	85.2	424	5	AAU79727	Aau79727 Human cyc
12	1903	84.8	432	4	AAU16967	Aau16967 Human nov
13	1787	79.7	336	5	ABB07912	Abb07912 Human PDE
14	1717	76.5	424	5	AAU79713	Aau79713 Human pho
15	1403.5	62.6	450	3	AAY93569	Aay93569 Amino aci
16	1403.5	62.6	450	4	AAU08675	Aau08675 Human pho
17	1403.5	62.6	450	4	AAG78915	Aag78915 Human typ
18	1391.5	62.0	446	3	AAY93567	Aay93567 Amino aci
19	1383.5	61.7	502	5	ABB09005	Abb09005 Human pho
20	1372.5	61.2	502	4	AAB36503	Aab36503 Human lon
21	1360.5	60.7	445	3	AAY93573	Aay93573 Amino aci
22	1358.5	60.6	446	3	AAY93574	Aay93574 Amino aci
23	1358	60.5	451	3	AAY93575	Aay93575 Amino aci
24	1338.5	59.7	437	3	AAY93572	Aay93572 Amino aci
25	1270.5	56.6	413	3	AAY93571	Aay93571 Amino aci
26	1221	54.4	391	4	AAU08676	Aau08676 Human pho
27	1079	48.1	211	4	AAU18681	Aau18681 Renal and
28	1079	48.1	211	4	AAU23004	Aau23004 Novel hum
29	1079	48.1	211	4	AAU17039	Aau17039 Human nov
30	1079	48.1	211	6	ABU97296	Abu97296 Human pol
31	891	39.7	268	3	AAY93593	Aay93593 Amino aci
32	891	39.7	288	3	AAY93568	Aay93568 Amino aci
33	871	38.8	320	4	AAB36504	Aab36504 Human sho
34	555	24.7	610	2	AAY27197	Aay27197 Rat PDE4A
35	551	24.6	721	6	ABP98434	Abp98434 Amino aci
36	550	24.5	562	2	AAR14836	Aar14836 "Dunce"-l
37	550	24.5	562	2	AAW00090	Aaw00090 Rat dunce
38	550	24.5	562	2	AAY49803	Aay49803 Rat dunce
39	550	24.5	562	3	AAB20614	Aab20614 Plasmid p
40	550	24.5	564	2	AAR60605	Aar60605 Brain low
41	550	24.5	564	2	AAY49825	Aay49825 Human dun
42	550	24.5	564	3	AAB20636	Aab20636 pPDE32 hu
43	550	24.5	564	3	AAY93994	Aay93994 Amino aci
44	550	24.5	564	4	AAE04745	Aae04745 Rat cAMP-
45	550	24.5	564	6	ABP96788	Abp96788 Human COP

ALIGNMENTS

RESULT 1
AAE24527
ID AAE24527 standard; protein; 426 AA.
XX
AC AAE24527;
XX
DT 04-OCT-2002 (first entry)
XX
DE Human PDE7 protein.
XX
KW Phosphodiesterase 7; PDE7; AIDS; acquired immune deficiency syndrome;
KW immune system disease; enzyme; chronic obstructive pulmonary disease;
KW T-cell related disease; autoimmune disorder; Crohn's disease; cancer;
KW rheumatoid arthritis; inflammatory disease; pancreatitis; leukaemia;
KW colitis; COPD; asthma; therapy; human.
XX
OS Homo sapiens.
XX
PN WO200226954-A2.
XX
PD 04-APR-2002.
XX
PF 28-SEP-2001; 2001WO-EP011303.
XX
PR 28-SEP-2000; 2000EP-00402683.
XX
PA (WARN) WARNER LAMBERT CO.
XX
PI Soulard P;
XX
DR WPI; 2002-479561/51.
DR N-PSDB; AAD39376.
XX
PT Novel polypeptides exhibiting a higher phosphodiesterase PDE7 activity
PT than endogenous full length PDE7, for screening of PDE7 inhibitors useful
PT in preventing and treating autoimmune disorders and inflammatory
PT diseases.
XX
PS Claim 2; Page 124-125; 137pp; English.
XX
CC The invention relates to novel polypeptides exhibiting a higher
CC phosphodiesterase 7 (PDE7) catalytic activity than endogenous full length
CC PDE7 and nucleic acid molecules encoding such polypeptides. Sequences of
CC the invention are used for screening compounds that inhibit PDE7
CC activity. PDE7 inhibitors are used for manufacturing a pharmaceutical
CC composition useful for the treatment or prevention of various
CC pathological conditions such as diseases affecting the immune system,
CC including acquired immune deficiency syndrome (AIDS), rejection of

```
CC   transplant, autoimmune disorders such as T-cells related diseases for
CC   e.g. rheumatoid arthritis, inflammatory diseases such as respiratory
CC   inflammation diseases including chronic obstructive pulmonary disease
CC   (COPD), asthma, gastrointestinal inflammation diseases such as Crohn's
CC   disease, colitis, pancreatitis and different types of cancers including
CC   leukaemia. The present sequence is human PDE7 protein
XX
SQ   Sequence 426 AA;

  Query Match             100.0%;  Score 2243;  DB 5;  Length 426;
  Best Local Similarity   100.0%;  Pred. No. 6.3e-226;
  Matches  426;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 DQTALYIRMLGDVRVRSRAGFESERRGSHPYIDFRIFHSQSEIEVSVSARNIRRLLSFQR 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 DQTALYIRMLGDVRVRSRAGFESERRGSHPYIDFRIFHSQSEIEVSVSARNIRRLLSFQR 60

Qy         61 YLRSSRFFRGTAVSNSLNILDDDYNGQAKCMLEKVGNWNFDIFLFDRLTNGNSLVSLTFH 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 YLRSSRFFRGTAVSNSLNILDDDYNGQAKCMLEKVGNWNFDIFLFDRLTNGNSLVSLTFH 120

Qy        121 LFSLHGLIEYFHLDMMKLRRFLVMIQEDYHSQNPYHNAVHAADVTQAMHCYLKEPKLANS 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 LFSLHGLIEYFHLDMMKLRRFLVMIQEDYHSQNPYHNAVHAADVTQAMHCYLKEPKLANS 180

Qy        181 VTPWDILLSLIAAATHDLDHPGVNQPFLIKTNHYLATLYKNTSVLENHHWRSAVGLLRES 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 VTPWDILLSLIAAATHDLDHPGVNQPFLIKTNHYLATLYKNTSVLENHHWRSAVGLLRES 240

Qy        241 GLFSHLPLESRQQMETQIGALILATDISRQNEYLSLFRSHLDRGDLCLEDTRHRHLVLQM 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GLFSHLPLESRQQMETQIGALILATDISRQNEYLSLFRSHLDRGDLCLEDTRHRHLVLQM 300

Qy        301 ALKCADICNPCRTWELSKQWSEKVTEEFFHQGDIEKKYHLGVSPLCDRHTESIANIQIGF 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 ALKCADICNPCRTWELSKQWSEKVTEEFFHQGDIEKKYHLGVSPLCDRHTESIANIQIGF 360

Qy        361 MTYLVEPLFTEWARFSNTRLSQTMLGHVGLNKASWKGLQREQSSSEDTDAAFELNSQLLP 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 MTYLVEPLFTEWARFSNTRLSQTMLGHVGLNKASWKGLQREQSSSEDTDAAFELNSQLLP 420

Qy        421 QENRLS 426
              ||||||
Db        421 QENRLS 426


RESULT 2
AAE24532
ID   AAE24532 standard; protein; 446 AA.
XX
AC   AAE24532;
XX
DT   04-OCT-2002  (first entry)
XX
DE   Human PDE7A2 protein.
XX
KW   Phosphodiesterase 7; PDE7A2; AIDS; acquired immune deficiency syndrome;
KW   immune system disease; enzyme; chronic obstructive pulmonary disease;
KW   T-cell related disease; autoimmune disorder; Crohn's disease; cancer;
KW   rheumatoid arthritis; inflammatory disease; pancreatitis; leukaemia;
KW   colitis; COPD; asthma; therapy; human.
XX
OS   Homo sapiens.
XX
PN   WO200226954-A2.
XX
PD   04-APR-2002.
XX
PF   28-SEP-2001; 2001WO-EP011303.
XX
PR   28-SEP-2000; 2000EP-00402683.
XX
PA   (WARN ) WARNER LAMBERT CO.
XX
PI   Soulard P;
XX
DR   WPI; 2002-479561/51.
XX
PT   Novel polypeptides exhibiting a higher phosphodiesterase PDE7 activity
PT   than endogenous full length PDE7, for screening of PDE7 inhibitors useful
PT   in preventing and treating autoimmune disorders and inflammatory
PT   diseases.
XX
PS   Disclosure; Fig 1; 137pp; English.
XX
CC   The invention relates to novel polypeptides exhibiting a higher
CC   phosphodiesterase 7 (PDE7) catalytic activity than endogenous full length
CC   PDE7 and nucleic acid molecules encoding such polypeptides. Sequences of
CC   the invention are used for screening compounds that inhibit PDE7
CC   activity. PDE7 inhibitors are used for manufacturing a pharmaceutical
CC   composition useful for the treatment or prevention of various
CC   pathological conditions such as diseases affecting the immune system,
CC   including acquired immune deficiency syndrome (AIDS), rejection of
CC   transplant, autoimmune disorders such as T-cells related diseases for
CC   e.g. rheumatoid arthritis, inflammatory diseases such as respiratory
CC   inflammation diseases including chronic obstructive pulmonary disease
CC   (COPD), asthma, gastrointestinal inflammation diseases such as Crohn's
CC   disease, colitis, pancreatitis and different types of cancers including
CC   leukaemia. The present sequence is human PDE7A2 protein
XX
SQ   Sequence 446 AA;

  Query Match             100.0%;  Score 2243;  DB 5;  Length 446;
  Best Local Similarity   100.0%;  Pred. No. 6.8e-226;
  Matches  426;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 DQTALYIRMLGDVRVRSRAGFESERRGSHPYIDFRIFHSQSEIEVSVSARNIRRLLSFQR 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         21 DQTALYIRMLGDVRVRSRAGFESERRGSHPYIDFRIFHSQSEIEVSVSARNIRRLLSFQR 80

Qy         61 YLRSSRFFRGTAVSNSLNILDDDYNGQAKCMLEKVGNWNFDIFLFDRLTNGNSLVSLTFH 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         81 YLRSSRFFRGTAVSNSLNILDDDYNGQAKCMLEKVGNWNFDIFLFDRLTNGNSLVSLTFH 140

Qy        121 LFSLHGLIEYFHLDMMKLRRFLVMIQEDYHSQNPYHNAVHAADVTQAMHCYLKEPKLANS 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        141 LFSLHGLIEYFHLDMMKLRRFLVMIQEDYHSQNPYHNAVHAADVTQAMHCYLKEPKLANS 200

Qy        181 VTPWDILLSLIAAATHDLDHPGVNQPFLIKTNHYLATLYKNTSVLENHHWRSAVGLLRES 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        201 VTPWDILLSLIAAATHDLDHPGVNQPFLIKTNHYLATLYKNTSVLENHHWRSAVGLLRES 260

Qy        241 GLFSHLPLESRQQMETQIGALILATDISRQNEYLSLFRSHLDRGDLCLEDTRHRHLVLQM 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        261 GLFSHLPLESRQQMETQIGALILATDISRQNEYLSLFRSHLDRGDLCLEDTRHRHLVLQM 320

Qy        301 ALKCADICNPCRTWELSKQWSEKVTEEFFHQGDIEKKYHLGVSPLCDRHTESIANIQIGF 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        321 ALKCADICNPCRTWELSKQWSEKVTEEFFHQGDIEKKYHLGVSPLCDRHTESIANIQIGF 380

Qy        361 MTYLVEPLFTEWARFSNTRLSQTMLGHVGLNKASWKGLQREQSSSEDTDAAFELNSQLLP 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        381 MTYLVEPLFTEWARFSNTRLSQTMLGHVGLNKASWKGLQREQSSSEDTDAAFELNSQLLP 440

Qy        421 QENRLS 426
              ||||||
Db        441 QENRLS 446


RESULT 3
AAE24531
ID   AAE24531 standard; protein; 482 AA.
XX
AC   AAE24531;
XX
DT   04-OCT-2002  (first entry)
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XX
DE   Human PDE7A1 protein.
XX
KW   Phosphodiesterase 7; PDE7A1; AIDS; acquired immune deficiency syndrome;
KW   immune system disease; enzyme; chronic obstructive pulmonary disease;
KW   T-cell related disease; autoimmune disorder; Crohn's disease; cancer;
KW   rheumatoid arthritis; inflammatory disease; pancreatitis; leukaemia;
KW   colitis; COPD; asthma; therapy; human.
XX
OS   Homo sapiens.
XX
PN   WO200226954-A2.
XX
PD   04-APR-2002.
XX
PF   28-SEP-2001; 2001WO-EP011303.
XX
PR   28-SEP-2000; 2000EP-00402683.
XX
PA   (WARN ) WARNER LAMBERT CO.
XX
PI   Soulard P;
XX
DR   WPI; 2002-479561/51.
XX
PT   Novel polypeptides exhibiting a higher phosphodiesterase PDE7 activity
PT   than endogenous full length PDE7, for screening of PDE7 inhibitors useful
PT   in preventing and treating autoimmune disorders and inflammatory
PT   diseases.
XX
PS   Disclosure; Fig 1; 137pp; English.
XX
CC   The invention relates to novel polypeptides exhibiting a higher
CC   phosphodiesterase 7 (PDE7) catalytic activity than endogenous full length
CC   PDE7 and nucleic acid molecules encoding such polypeptides. Sequences of
CC   the invention are used for screening compounds that inhibit PDE7
CC   activity. PDE7 inhibitors are used for manufacturing a pharmaceutical
CC   composition useful for the treatment or prevention of various
CC   pathological conditions such as diseases affecting the immune system,
CC   including acquired immune deficiency syndrome (AIDS), rejection of
CC   transplant, autoimmune disorders such as T-cells related diseases for
CC   e.g. rheumatoid arthritis, inflammatory diseases such as respiratory
CC   inflammation diseases including chronic obstructive pulmonary disease
CC   (COPD), asthma, gastrointestinal inflammation diseases such as Crohn's
CC   disease, colitis, pancreatitis and different types of cancers including
CC   leukaemia. The present sequence is human PDE7A1 protein
XX
SQ   Sequence 482 AA;

  Query Match             100.0%;  Score 2243;  DB 5;  Length 482;
  Best Local Similarity   100.0%;  Pred. No. 7.7e-226;
  Matches  426;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 DQTALYIRMLGDVRVRSRAGFESERRGSHPYIDFRIFHSQSEIEVSVSARNIRRLLSFQR 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         57 DQTALYIRMLGDVRVRSRAGFESERRGSHPYIDFRIFHSQSEIEVSVSARNIRRLLSFQR 116

Qy         61 YLRSSRFFRGTAVSNSLNILDDDYNGQAKCMLEKVGNWNFDIFLFDRLTNGNSLVSLTFH 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        117 YLRSSRFFRGTAVSNSLNILDDDYNGQAKCMLEKVGNWNFDIFLFDRLTNGNSLVSLTFH 176

Qy        121 LFSLHGLIEYFHLDMMKLRRFLVMIQEDYHSQNPYHNAVHAADVTQAMHCYLKEPKLANS 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        177 LFSLHGLIEYFHLDMMKLRRFLVMIQEDYHSQNPYHNAVHAADVTQAMHCYLKEPKLANS 236

Qy        181 VTPWDILLSLIAAATHDLDHPGVNQPFLIKTNHYLATLYKNTSVLENHHWRSAVGLLRES 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        237 VTPWDILLSLIAAATHDLDHPGVNQPFLIKTNHYLATLYKNTSVLENHHWRSAVGLLRES 296

Qy        241 GLFSHLPLESRQQMETQIGALILATDISRQNEYLSLFRSHLDRGDLCLEDTRHRHLVLQM 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        297 GLFSHLPLESRQQMETQIGALILATDISRQNEYLSLFRSHLDRGDLCLEDTRHRHLVLQM 356

Qy        301 ALKCADICNPCRTWELSKQWSEKVTEEFFHQGDIEKKYHLGVSPLCDRHTESIANIQIGF 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        357 ALKCADICNPCRTWELSKQWSEKVTEEFFHQGDIEKKYHLGVSPLCDRHTESIANIQIGF 416

Qy        361 MTYLVEPLFTEWARFSNTRLSQTMLGHVGLNKASWKGLQREQSSSEDTDAAFELNSQLLP 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        417 MTYLVEPLFTEWARFSNTRLSQTMLGHVGLNKASWKGLQREQSSSEDTDAAFELNSQLLP 476

Qy        421 QENRLS 426
              ||||||
Db        477 QENRLS 482


RESULT 4
AAW00094
ID   AAW00094 standard; protein; 498 AA.
XX
AC   AAW00094;
XX
DT   25-MAR-2003  (revised)
DT   09-OCT-1996  (first entry)
XX
DE   cAMP phosphodiesterase encoded by plasmid pTM22 (ATCC 68601).
XX
KW   Human; glioblastoma cell; heat shock sensitivity; phosphodiesterase;
KW   deficient yeast strain 10DAB; pTM22; rat DPD phosphodiesterase; pde1-;
KW   bovine Ca2+/calmodulin dependent cAMP phosphodiesterase; heart; plasmid;
KW   RAS2(val19); pde2-; pTM3; pTM72; pRATDPD; pJC99; rolipram sensitive.
XX
OS   Homo sapiens.
XX
PN   US5527896-A.
XX
PD   18-JUN-1996.
XX
PF   19-APR-1991;   91US-00688352.
XX
PR   20-APR-1990;   90US-00511715.
XX
PA   (COLD-) COLD SPRING HARBOR LAB.
XX
PI   Colicelli JJ,  Wigler MH;
XX
DR   WPI; 1996-299902/30.
DR   N-PSDB; AAT34376.
XX
PT   DNA mols. isolated from human glioblastoma cells - encode RAS-related or
PT   cyclic nucleotide phosphodiesterase proteins.
XX
PS   Claim 4; Col 67-70; 101pp; English.
XX
CC   The sequences given in AAW00092-94 are encoded by plasmid fragments which
CC   contain human glioblastoma cell cDNA inserts which are capable of
CC   correcting the heat shock sensitivity of the phosphodiesterase deficient
CC   yeast strain 10DAB. Several cDNA's were isolated and sequenced. pTM22
CC   encodes a novel human gene. From computer analysis, pTM22 putatively
CC   encodes a protein homologous to various cAMP phosphodiesterases, such as
CC   the bovine Ca2+/calmodulin dependent cAMP phosphodiesterase and the rat
CC   DPD phosphodiesterase. Sequences related to pTM22 were found to be
CC   expressed in human heart. Plasmid pTM22 was unable to correct the heat
CC   shock sensitivity of RAS2(val19) yeast strains. It thus appears that the
CC   pde1- and pde2- yeast strain 10DAB is more sensitive to phenotypic
CC   reversion by mammalian cAMP phosphodiesterase clones than is the
CC   RAS2(val19) yeast strain. The inserts in the plasmids pTM3 and pTM72 were
CC   also characterised. These two different cAMP phosphodiesterase cDNA's
CC   were found to be closely related to, but distinct from, the pRATDPD
CC   insert and the pJC99 insert. Biochemical analysis of cell lysates has
CC   established that the cDNA's of pTM3 and pTM72, pJC44x and pRATDPD encode
CC   rolipram sensitive cAMP phosphodiesterases. (Updated on 25-MAR-2003 to
CC   correct PF field.)
XX
SQ   Sequence 498 AA;
```

```
  Query Match             100.0%;  Score 2243;  DB 2;  Length 498;
  Best Local Similarity   100.0%;  Pred. No. 8.1e-226;
  Matches  426;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 DQTALYIRMLGDVRVRSRAGFESERRGSHPYIDFRIFHSQSEIEVSVSARNIRRLLSFQR 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         73 DQTALYIRMLGDVRVRSRAGFESERRGSHPYIDFRIFHSQSEIEVSVSARNIRRLLSFQR 132

Qy         61 YLRSSRFFRGTAVSNSLNILDDDYNGQAKCMLEKVGNWNFDIFLFDRLTNGNSLVSLTFH 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        133 YLRSSRFFRGTAVSNSLNILDDDYNGQAKCMLEKVGNWNFDIFLFDRLTNGNSLVSLTFH 192

Qy        121 LFSLHGLIEYFHLDMMKLRRFLVMIQEDYHSQNPYHNAVHAADVTQAMHCYLKEPKLANS 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        193 LFSLHGLIEYFHLDMMKLRRFLVMIQEDYHSQNPYHNAVHAADVTQAMHCYLKEPKLANS 252

Qy        181 VTPWDILLSLIAAATHDLDHPGVNQPFLIKTNHYLATLYKNTSVLENHHWRSAVGLLRES 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        253 VTPWDILLSLIAAATHDLDHPGVNQPFLIKTNHYLATLYKNTSVLENHHWRSAVGLLRES 312

Qy        241 GLFSHLPLESRQQMETQIGALILATDISRQNEYLSLFRSHLDRGDLCLEDTRHRHLVLQM 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        313 GLFSHLPLESRQQMETQIGALILATDISRQNEYLSLFRSHLDRGDLCLEDTRHRHLVLQM 372

Qy        301 ALKCADICNPCRTWELSKQWSEKVTEEFFHQGDIEKKYHLGVSPLCDRHTESIANIQIGF 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        373 ALKCADICNPCRTWELSKQWSEKVTEEFFHQGDIEKKYHLGVSPLCDRHTESIANIQIGF 432

Qy        361 MTYLVEPLFTEWARFSNTRLSQTMLGHVGLNKASWKGLQREQSSSEDTDAAFELNSQLLP 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        433 MTYLVEPLFTEWARFSNTRLSQTMLGHVGLNKASWKGLQREQSSSEDTDAAFELNSQLLP 492

Qy        421 QENRLS 426
              ||||||
Db        493 QENRLS 498
```

```
RESULT 5
AAY49808
ID   AAY49808 standard; protein; 498 AA.
XX
AC   AAY49808;
XX
DT   19-JAN-2000  (first entry)
XX
DE   Human glioblastoma cell cAMP phosphodiesterase pTM22 protein.
XX
KW   Phosphodiesterase; dunce-like phosphodiesterase; PDE; DPD; cAMP;
KW   RAS-related protein; immunoreactive; detection; genetic defect;
KW   bronchodilation; increased myocardial contractility; anti-inflammation.
XX
OS   Homo sapiens.
XX
PN   US5977305-A.
XX
PD   02-NOV-1999.
XX
PF   07-JUN-1995;   95US-00474379.
XX
PR   20-APR-1990;   90US-00511715.
PR   19-APR-1991;   91US-00688352.
PR   01-MAR-1994;   94US-00206188.
XX
PA   (COLD-) COLD SPRING HARBOR LAB.
XX
PI   Colicelli JJ,  Wigler MH;
XX
DR   WPI; 1999-619709/53.
DR   N-PSDB; AAZ32240.
XX
PT   New isolated RAS-related polypeptides and mammalian cyclic nucleotide
PT   phosphodiesterases, used for screening for agents which can modify
PT   complement or suppress genetic defects.
XX
PS   Claim 2; Col 85-88; 145pp; English.
XX
CC   The present invention describes new isolated RAS-related polypeptides and
CC   mammalian cyclic nucleotide phosphodiesterases (PDEs). RAS-related
CC   polypeptides are capable of complementing a defective RAS function in
CC   yeast. The products can be used for screening for agents which can
CC   modify, complement or suppress a genetic defect in a biochemical pathway
CC   in which cAMP participates, or in a biochemical pathway which is
CC   controlled, directly or indirectly, by a RAS protein and other proteins
CC   affecting cell growth and maintenance. Developing agents that will
CC   selectively act upon PDEs is directed toward reproducing the desirable
CC   effects of cyclic nucleotides, e.g. bronchodilation, increased myocardial
CC   contractility, anti-inflammation, yet without causing the undesirable
CC   effects, e.g. increased heart rate or enhanced lipolysis. The products
CC   can also be used for therapeutic, diagnostic and prognostic uses.
CC   AAZ32229 to AAZ32285, and AAY49803 to AAY49830, represent sequences used
CC   in the exemplification of the present invention
XX
SQ   Sequence 498 AA;
```

```
  Query Match             100.0%;  Score 2243;  DB 2;  Length 498;
  Best Local Similarity   100.0%;  Pred. No. 8.1e-226;
  Matches  426;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 DQTALYIRMLGDVRVRSRAGFESERRGSHPYIDFRIFHSQSEIEVSVSARNIRRLLSFQR 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         73 DQTALYIRMLGDVRVRSRAGFESERRGSHPYIDFRIFHSQSEIEVSVSARNIRRLLSFQR 132

Qy         61 YLRSSRFFRGTAVSNSLNILDDDYNGQAKCMLEKVGNWNFDIFLFDRLTNGNSLVSLTFH 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        133 YLRSSRFFRGTAVSNSLNILDDDYNGQAKCMLEKVGNWNFDIFLFDRLTNGNSLVSLTFH 192

Qy        121 LFSLHGLIEYFHLDMMKLRRFLVMIQEDYHSQNPYHNAVHAADVTQAMHCYLKEPKLANS 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        193 LFSLHGLIEYFHLDMMKLRRFLVMIQEDYHSQNPYHNAVHAADVTQAMHCYLKEPKLANS 252

Qy        181 VTPWDILLSLIAAATHDLDHPGVNQPFLIKTNHYLATLYKNTSVLENHHWRSAVGLLRES 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        253 VTPWDILLSLIAAATHDLDHPGVNQPFLIKTNHYLATLYKNTSVLENHHWRSAVGLLRES 312

Qy        241 GLFSHLPLESRQQMETQIGALILATDISRQNEYLSLFRSHLDRGDLCLEDTRHRHLVLQM 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        313 GLFSHLPLESRQQMETQIGALILATDISRQNEYLSLFRSHLDRGDLCLEDTRHRHLVLQM 372

Qy        301 ALKCADICNPCRTWELSKQWSEKVTEEFFHQGDIEKKYHLGVSPLCDRHTESIANIQIGF 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        373 ALKCADICNPCRTWELSKQWSEKVTEEFFHQGDIEKKYHLGVSPLCDRHTESIANIQIGF 432

Qy        361 MTYLVEPLFTEWARFSNTRLSQTMLGHVGLNKASWKGLQREQSSSEDTDAAFELNSQLLP 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        433 MTYLVEPLFTEWARFSNTRLSQTMLGHVGLNKASWKGLQREQSSSEDTDAAFELNSQLLP 492

Qy        421 QENRLS 426
              ||||||
Db        493 QENRLS 498
```

```
RESULT 6
AAB20619
ID   AAB20619 standard; protein; 498 AA.
XX
AC   AAB20619;
XX
DT   14-DEC-2000  (first entry)
XX
DE   pTM22 human glioblastoma cell insert protein sequence SEQ ID NO:20.
XX
KW   Detection; mammalian gene; yeast; microorganism; identification;
KW   phenotype; characteristic; dunce-like phosphodiesterase; PDE; RAS;
KW   RAS-related protein; genetic defect; hybridisation; probe.
XX
OS   Homo sapiens.
```

OS Saccharomyces cerevisiae.
XX
PN US6100025-A.
XX
PD 08-AUG-2000.
XX
PF 01-MAR-1994; 94US-00206188.
XX
PR 20-APR-1990; 90US-00511715.
PR 19-APR-1991; 91US-00688352.
XX
PA (COLD-) COLD SPRING HARBOR LAB.
XX
PI Colicelli JJ, Wigler MH;
XX
DR WPI; 2000-531664/48.
DR N-PSDB; AAA88175.
XX
PT Novel isolated DNA encoding a mammalian cyclic nucleotide
PT phosphodiesterase is present in plasmids pPDE46, pPDE43 or pPDE339 and is
PT used to modify a genetic defect in a biochemical pathway in which cAMP
PT participates.
XX
PS Example 1; Col 85-88; 145pp; English.
XX
CC The present invention describes a purified and isolated DNA (I) which
CC encodes a mammalian cyclic nucleotide phosphodiesterase and is an insert
CC present in the plasmids pPDE46 (ATCC 69552), pPDE43 (ATCC 69551) or
CC pPDE339 (ATCC 69550). The DNA molecules are used to modify, complement or
CC suppress a genetic defect in a biochemical pathway in which cAMP
CC participates and are also used as hybridisation probes. The present
CC invention also describes methods for detecting mammalian genes encoding
CC proteins which can function in microorganisms, particularly yeast, to
CC modify, complement, or suppress a genetic defect associated with an
CC identifiable phenotypic alteration or characteristic in the
CC microorganism. AAA88162 to AAA88218 and AAB29614 to AAB20640 represent
CC sequences used in the exemplification of the present invention
XX
SQ Sequence 498 AA;

Query Match 100.0%; Score 2243; DB 3; Length 498;
Best Local Similarity 100.0%; Pred. No. 8.1e-226;
Matches 426; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DQTALYIRMLGDVRVRSRAGFESERRGSHPYIDFRIFHSQSEIEVSVSARNIRRLLSFQR 60
Db 73 DQTALYIRMLGDVRVRSRAGFESERRGSHPYIDFRIFHSQSEIEVSVSARNIRRLLSFQR 132

Qy 61 YLRSSRFFRGTAVSNSLNILDDDYNGQAKCMLEKVGNWNFDIFLFDRLTNGNSLVSLTFH 120
Db 133 YLRSSRFFRGTAVSNSLNILDDDYNGQAKCMLEKVGNWNFDIFLFDRLTNGNSLVSLTFH 192

Qy 121 LFSLHGLIEYFHLDMMKLRRFLVMIQEDYHSQNPYHNAVHAADVTQAMHCYLKEPKLANS 180
Db 193 LFSLHGLIEYFHLDMMKLRRFLVMIQEDYHSQNPYHNAVHAADVTQAMHCYLKEPKLANS 252

Qy 181 VTPWDILLSLIAAATHDLDHPGVNQPFLIKTNHYLATLYKNTSVLENHHWRSAVGLLRES 240
Db 253 VTPWDILLSLIAAATHDLDHPGVNQPFLIKTNHYLATLYKNTSVLENHHWRSAVGLLRES 312

Qy 241 GLFSHLPLESRQQMETQIGALILATDISRQNEYLSLFRSHLDRGDLCLEDTRHRHLVLQM 300
Db 313 GLFSHLPLESRQQMETQIGALILATDISRQNEYLSLFRSHLDRGDLCLEDTRHRHLVLQM 372

Qy 301 ALKCADICNPCRTWELSKQWSEKVTEEFFHQGDIEKKYHLGVSPLCDRHTESIANIQIGF 360
Db 373 ALKCADICNPCRTWELSKQWSEKVTEEFFHQGDIEKKYHLGVSPLCDRHTESIANIQIGF 432

Qy 361 MTYLVEPLFTEWARFSNTRLSQTMLGHVGLNKASWKGLQREQSSSEDTDAAPELNSQLLP 420
Db 433 MTYLVEPLFTEWARFSNTRLSQTMLGHVGLNKASWKGLQREQSSSEDTDAAPELNSQLLP 492

Qy 421 QENRLS 426
Db 493 QENRLS 498

RESULT 7
AAE24529
ID AAE24529 standard; protein; 426 AA.
XX
AC AAE24529;
XX
DT 04-OCT-2002 (first entry)
XX
DE Rat PDE7 protein.
XX
KW Phosphodiesterase 7; PDE7; AIDS; acquired immune deficiency syndrome;
KW immune system disease; enzyme; chronic obstructive pulmonary disease;
KW T-cell related disease; autoimmune disorder; Crohn's disease; cancer;
KW rheumatoid arthritis; inflammatory disease; pancreatitis; leukaemia;
KW colitis; COPD; asthma; therapy; rat.
XX
OS Rattus sp.
XX
PN WO200226954-A2.
XX
PD 04-APR-2002.
XX
PF 28-SEP-2001; 2001WO-EP011303.
XX
PR 28-SEP-2000; 2000EP-00402683.
XX
PA (WARN) WARNER LAMBERT CO.
XX
PI Soulard P;
XX
DR WPI; 2002-479561/51.
DR N-PSDB; AAD39378.
XX
PT Novel polypeptides exhibiting a higher phosphodiesterase PDE7 activity
PT than endogenous full length PDE7, for screening of PDE7 inhibitors useful
PT in preventing and treating autoimmune disorders and inflammatory
PT diseases.
XX
PS Claim 2; Page 127-128; 137pp; English.
XX
CC The invention relates to novel polypeptides exhibiting a higher
CC phosphodiesterase 7 (PDE7) catalytic activity than endogenous full length
CC PDE7 and nucleic acid molecules encoding such polypeptides. Sequences of
CC the invention are used for screening compounds that inhibit PDE7
CC activity. PDE7 inhibitors are used for manufacturing a pharmaceutical
CC composition useful for the treatment or prevention of various
CC pathological conditions such as diseases affecting the immune system,
CC including acquired immune deficiency syndrome (AIDS), rejection of
CC transplant, autoimmune disorders such as T-cells related diseases for
CC e.g. rheumatoid arthritis, inflammatory diseases such as respiratory
CC inflammation diseases including chronic obstructive pulmonary disease
CC (COPD), asthma, gastrointestinal inflammation diseases such as Crohn's
CC disease, colitis, pancreatitis and different types of cancers including
CC leukaemia. The present sequence is rat PDE7 protein
XX
SQ Sequence 426 AA;

Query Match 94.3%; Score 2116; DB 5; Length 426;
Best Local Similarity 94.1%; Pred. No. 1.3e-212;
Matches 401; Conservative 9; Mismatches 16; Indels 0; Gaps 0;

Qy 1 DQTALYIRMLGDVRVRSRAGFESERRGSHPYIDFRIFHSQSEIEVSVSARNIRRLLSFQR 60
Db 1 DQTALYIRMLGDVRVRSRAGFETERRGSHPYIDFRIFHAQSEIEASVSARNIRRLLSFQR 60

Qy 61 YLRSSRFFRGTAVSNSLNILDDDYNGQAKCMLEKVGNWNFDIFLFDRLTNGNSLVSLTFH 120
Db 61 YLRSSRFFRGATVCRSLNILDEDYNGQAKCMLEKVGNWNFDIFLFDRLTNGNSLVSLTFH 120

```
Qy        121 LFSLHGLIEYFHLDMMKLRRFLVMIQEDYHSQNPYHNAVHAADVTQAMHCYLKEPKLANS 180
              ||||||||||||||:||||||||||||||||||||||||||||||||||||||||||||||
Db        121 LFSLHGLIEYFHLDMVKLRRFLVMIQEDYHSQNPYHNAVHAADVTQAMHCYLKEPKLANS 180

Qy        181 VTPWDILLSLIAAATHDLDHPGVNQPFLIKTNHYLATLYKNTSVLENHHWRSAVGLLRES 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 VTPWDILLSLIAAATHDLDHPGVNQPFLIKTNHYLATLYKNTSVLENHHWRSAVGLLRES 240

Qy        241 GLFSHLPLESRQQMETQIGALILATDISRQNEYLSLFRSHLDRGDLCLEDTRHRHLVLQM 300
              |||||||||||  :|| |||||||||||||||||||||||:||| |:| |||||||||
Db        241 GLFSHLPLESRHEMEAQIGALILATDISRQNEYLSLFRSHLDKGDLHLDDGRHRHLVLQM 300

Qy        301 ALKCADICNPCRTWELSKQWSEKVTEEFFHQGDIEKKYHLGVSPLCDRHTESIANIQIGF 360
              ||||||||||| |||||||||||||||||||||||||||||||| ||||||||||
Db        301 ALKCADICNPCRNWELSKQWSEKVTEEFFHQGDIEKKYHLGVSPLCDRQTESIANIQIGF 360

Qy        361 MTYLVEPLFTEWARFSNTRLSQTMLGHVGLNKASWKGLQREQSSSEDTDAAFELNSQLLP 420
              |||| ||||||||||:||||||||||||||||||:| |||| ||||||||||
Db        361 MTYLQEPLFTEWARFSDTRLSQTMLGHVGLNKASWKGLQRQQPSSEDASAAFELNSQLLT 420

Qy        421 QENRLS 426
              ||||||
Db        421 QENRLS 426
```

RESULT 8
AAE24533
ID AAE24533 standard; protein; 428 AA.
XX
AC AAE24533;
XX
DT 04-OCT-2002 (first entry)
XX
DE Rat PDE7a protein.
XX
KW Phosphodiesterase 7; PDE7a; AIDS; acquired immune deficiency syndrome;
KW immune system disease; enzyme; chronic obstructive pulmonary disease;
KW T-cell related disease; autoimmune disorder; Crohn's disease; cancer;
KW rheumatoid arthritis; inflammatory disease; pancreatitis; leukaemia;
KW colitis; COPD; asthma; therapy; rat.
XX
OS Rattus sp.
XX
PN WO200226954-A2.
XX
PD 04-APR-2002.
XX
PF 28-SEP-2001; 2001WO-EP011303.
XX
PR 28-SEP-2000; 2000EP-00402683.
XX
PA (WARN) WARNER LAMBERT CO.
XX
PI Soulard P;
XX
DR WPI; 2002-479561/51.
XX
PT Novel polypeptides exhibiting a higher phosphodiesterase PDE7 activity
PT than endogenous full length PDE7, for screening of PDE7 inhibitors useful
PT in preventing and treating autoimmune disorders and inflammatory
PT diseases.
XX
PS Disclosure; Fig 1; 137pp; English.
XX
CC The invention relates to novel polypeptides exhibiting a higher
CC phosphodiesterase 7 (PDE7) catalytic activity than endogenous full length
CC PDE7 and nucleic acid molecules encoding such polypeptides. Sequences of
CC the invention are used for screening compounds that inhibit PDE7
CC activity. PDE7 inhibitors are used for manufacturing a pharmaceutical
CC composition useful for the treatment or prevention of various
CC pathological conditions such as diseases affecting the immune system,
CC including acquired immune deficiency syndrome (AIDS), rejection of
CC transplant, autoimmune disorders such as T-cells related diseases for
CC e.g. rheumatoid arthritis, inflammatory diseases such as respiratory
CC inflammation diseases including chronic obstructive pulmonary disease
CC (COPD), asthma, gastrointestinal inflammation diseases such as Crohn's
CC disease, colitis, pancreatitis and different types of cancers including
CC leukaemia. The present sequence is rat PDE7a protein
XX
SQ Sequence 428 AA;

```
  Query Match             94.3%;  Score 2116;  DB 5;  Length 428;
  Best Local Similarity   94.1%;  Pred. No. 1.3e-212;
  Matches  401;  Conservative    9;  Mismatches   16;  Indels    0;  Gaps    0;

Qy          1 DQTALYIRMLGDVRVRSRAGFESERRGSHPYIDFRIFHSQSEIEVSVSARNIRRLLSFQR 60
              |||||||||||||||||||:|||||||||||||:||||| ||||||||||||||
Db          3 DQTALYIRMLGDVRVRSRAGFETERRGSHPYIDFRIFHAQSEIEASVSARNIRRLLSFQR 62

Qy         61 YLRSSRFFRGTAVSNSLNILDDDYNGQAKCMLEKVGNWNFDIFLFDRLTNGNSLVSLTFH 120
              ||||||||||  |  ||||||:|||||||||||||||||||||||||||||||||||||
Db         63 YLRSSRFFRGATVCRSLNILDEDYNGQAKCMLEKVGNWNFDIFLFDRLTNGNSLVSLTFH 122

Qy        121 LFSLHGLIEYFHLDMMKLRRFLVMIQEDYHSQNPYHNAVHAADVTQAMHCYLKEPKLANS 180
              |||||||||||||:|||||||||||||||||||||||||||||||||||||||||||||||
Db        123 LFSLHGLIEYFHLDMVKLRRFLVMIQEDYHSQNPYHNAVHAADVTQAMHCYLKEPKLANS 182

Qy        181 VTPWDILLSLIAAATHDLDHPGVNQPFLIKTNHYLATLYKNTSVLENHHWRSAVGLLRES 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        183 VTPWDILLSLIAAATHDLDHPGVNQPFLIKTNHYLATLYKNTSVLENHHWRSAVGLLRES 242

Qy        241 GLFSHLPLESRQQMETQIGALILATDISRQNEYLSLFRSHLDRGDLCLEDTRHRHLVLQM 300
              |||||||||||  :|| |||||||||||||||||||||||:||| |:| |||||||||
Db        243 GLFSHLPLESRHEMEAQIGALILATDISRQNEYLSLFRSHLDKGDLHLDDGRHRHLVLQM 302

Qy        301 ALKCADICNPCRTWELSKQWSEKVTEEFFHQGDIEKKYHLGVSPLCDRHTESIANIQIGF 360
              ||||||||||| |||||||||||||||||||||||||||||||| ||||||||||
Db        303 ALKCADICNPCRNWELSKQWSEKVTEEFFHQGDIEKKYHLGVSPLCDRQTESIANIQIGF 362

Qy        361 MTYLVEPLFTEWARFSNTRLSQTMLGHVGLNKASWKGLQREQSSSEDTDAAFELNSQLLP 420
              |||| ||||||||||:||||||||||||||||||:| |||| ||||||||||
Db        363 MTYLQEPLFTEWARFSDTRLSQTMLGHVGLNKASWKGLQRQQPSSEDASAAFELNSQLLT 422

Qy        421 QENRLS 426
              ||||||
Db        423 QENRLS 428
```

RESULT 9
AAE24528
ID AAE24528 standard; protein; 426 AA.
XX
AC AAE24528;
XX
DT 04-OCT-2002 (first entry)
XX
DE Mouse PDE7 protein.
XX
KW Phosphodiesterase 7; PDE7; AIDS; acquired immune deficiency syndrome;
KW immune system disease; enzyme; chronic obstructive pulmonary disease;
KW T-cell related disease; autoimmune disorder; Crohn's disease; cancer;
KW rheumatoid arthritis; inflammatory disease; pancreatitis; leukaemia;
KW colitis; COPD; asthma; therapy; mouse.
XX
OS Mus sp.
XX
FH Key   Location/Qualifiers
FT Misc-difference 23
FT   /note= "Encoded by TCA"
FT Misc-difference 42
FT   /note= "Encoded by GAA"
FT Misc-difference 45
FT   /note= "Encoded by GTG"
FT Misc-difference 67
FT   /note= "Encoded by TTT"
FT Misc-difference 71

```
FT                   /note= "Encoded by ACT"
FT   Misc-difference 72
FT                   /note= "Encoded by GCG"
FT   Misc-difference 74
FT                   /note= "Encoded by TCA"
FT   Misc-difference 75
FT                   /note= "Encoded by AAT"
FT   Misc-difference 78
FT                   /note= "Encoded by AAC"
FT   Misc-difference 82
FT                   /note= "Encoded by GAT"
FT   Misc-difference 136
FT                   /note= "Encoded by ATG"
FT   Misc-difference 179
FT                   /note= "Encoded by AAT"
FT   Misc-difference 222
FT                   /note= "Encoded by ACC"
FT   Misc-difference 253
FT                   /note= "Encoded by CAA"
FT   Misc-difference 256
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FT   Misc-difference 289
FT                   /note= "Encoded by GAA"
FT   Misc-difference 291
FT                   /note= "Encoded by ACC"
FT   Misc-difference 313
FT                   /note= "Encoded by ACG"
FT   Misc-difference 349
FT                   /note= "Encoded by CAC"
FT   Misc-difference 377
FT                   /note= "Encoded by AAT"
FT   Misc-difference 401
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FT   Misc-difference 403
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FT   Misc-difference 409
FT                   /note= "Encoded by GAT"
FT   Misc-difference 420
FT                   /note= "Encoded by CCT"
XX
PN   WO200226954-A2.
XX
PD   04-APR-2002.
XX
PF   28-SEP-2001; 2001WO-EP011303.
XX
PR   28-SEP-2000; 2000EP-00402683.
XX
PA   (WARN ) WARNER LAMBERT CO.
XX
PI   Soulard P;
XX
DR   WPI; 2002-479561/51.
DR   N-PSDB; AAD39377.
XX
PT   Novel polypeptides exhibiting a higher phosphodiesterase PDE7 activity
PT   than endogenous full length PDE7, for screening of PDE7 inhibitors useful
PT   in preventing and treating autoimmune disorders and inflammatory
PT   diseases.
XX
PS   Claim 2; Page 125-127; 137pp; English.
XX
CC   The invention relates to novel polypeptides exhibiting a higher
CC   phosphodiesterase 7 (PDE7) catalytic activity than endogenous full length
CC   PDE7 and nucleic acid molecules encoding such polypeptides. Sequences of
CC   the invention are used for screening compounds that inhibit PDE7
CC   activity. PDE7 inhibitors are used for manufacturing a pharmaceutical
CC   composition useful for the treatment or prevention of various
CC   pathological conditions such as diseases affecting the immune system,
CC   including acquired immune deficiency syndrome (AIDS), rejection of
CC   transplant, autoimmune disorders such as T-cells related diseases for
CC   e.g. rheumatoid arthritis, inflammatory diseases such as respiratory
CC   inflammation diseases including chronic obstructive pulmonary disease
CC   (COPD), asthma, gastrointestinal inflammation diseases such as Crohn's
CC   disease, colitis, pancreatitis and different types of cancers including
CC   leukaemia. The present sequence is mouse PDE7 protein
XX
SQ   Sequence 426 AA;

  Query Match             93.8%;  Score 2105;  DB 5;  Length 426;
  Best Local Similarity   93.7%;  Pred. No. 1.9e-211;
  Matches  399;  Conservative   13;  Mismatches   14;  Indels    0;  Gaps    0;

Qy          1 DQTALYIRMLGDVRVRSRAGFESERRGSHPYIDFRIFHSQSEIEVSVSARNIRRLLSFQR 60
              ||||||||||||||||||||||:||||||||||||||||:|| ||||||||||||||||
Db          1 DQTALYIRMLGDVRVRSRAGFETERRGSHPYIDFRIFHSQSDIEASVSARNIRRLLSFQR 60

Qy         61 YLRSSRFFRGTAVSNSLNILDDDYNGQAKCMLEKVGNWNFDIFLFDRLTNGNSLVSLTFH 120
              |||||| ||| | :||:|||:|||||||||||||||||||||||||||||||||||||||
Db         61 YLRSSRVFRGATVCSSLDILDEDYNGQAKCMLEKVGNWNFDIFLFDRLTNGNSLVSLTFH 120

Qy        121 LFSLHGLIEYFHLDMMKLRRFLVMIQEDYHSQNPYHNAVHAADVTQAMHCYLKEPKLANS 180
              |||||||||||||||:|||||||||||||||||||||||||||||||||||||||||||:|
Db        121 LFSLHGLIEYFHLDMVKLRRFLVMIQEDYHSQNPYHNAVHAADVTQAMHCYLKEPKLASS 180

Qy        181 VTPWDILLSLIAAATHDLDHPGVNQPFLIKTNHYLATLYKNTSVLENHHWRSAVGLLRES 240
              ||||||||||||||||||||||||||||||||||||||||:||||||||||||||||||
Db        181 VTPWDILLSLIAAATHDLDHPGVNQPFLIKTNHYLATLYKNSSVLENHHWRSAVGLLRES 240

Qy        241 GLFSHLPLESRQQMETQIGALILATDISRQNEYLSLFRSHLDRGDLCLEDTRHRHLVLQM 300
              |||||||||||:|| ||||||||||||||||||||||:|| |:| |||||||||
Db        241 GLFSHLPLESRQEMEAQIGALILATDISRQNEYLSLFRSHLDKGDLHLDDGRHRHLVLQM 300

Qy        301 ALKCADICNPCRTWELSKQWSEKVTEEFFHQGDIEKKYHLGVSPLCDRHTESIANIQIGF 360
              |||||||||||| ||||||||||||||||||||||||||||||||| ||||||||||
Db        301 ALKCADICNPCRNWELSKQWSEKVTEEFFHQGDIEKKYHLGVSPLCDRQTESIANIQIGF 360

Qy        361 MTYLVEPLFTEWARFSNTRLSQTMLGHVGLNKASWKGLQREQSSSSEDTDAAFELNSQLLP 420
              |||||||||||||||| ||||||||||||||||||||:| |||| :||||||||||
Db        361 MTYLVEPLFTEWARFSATRLSQTMLGHVGLNKASWKGLQRQQPSSEDANAAFELNSQLLT 420

Qy        421 QENRLS 426
              ||||||
Db        421 QENRLS 426


RESULT 10
AAE24530
ID   AAE24530 standard; protein; 456 AA.
XX
AC   AAE24530;
XX
DT   04-OCT-2002  (first entry)
XX
DE   Mouse PDE7A2 protein.
XX
KW   Phosphodiesterase 7; PDE7A2; AIDS; acquired immune deficiency syndrome;
KW   immune system disease; enzyme; chronic obstructive pulmonary disease;
KW   T-cell related disease; autoimmune disorder; Crohn's disease; cancer;
KW   rheumatoid arthritis; inflammatory disease; pancreatitis; leukaemia;
KW   colitis; COPD; asthma; therapy; mouse.
XX
OS   Mus sp.
XX
PN   WO200226954-A2.
XX
PD   04-APR-2002.
XX
PF   28-SEP-2001; 2001WO-EP011303.
XX
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PR   28-SEP-2000; 2000EP-00402683.
XX
PA   (WARN ) WARNER LAMBERT CO.
XX
PI   Soulard P;
XX
DR   WPI; 2002-479561/51.
DR   N-PSDB; AAD39383.
XX
PT   Novel polypeptides exhibiting a higher phosphodiesterase PDE7 activity
PT   than endogenous full length PDE7, for screening of PDE7 inhibitors useful
PT   in preventing and treating autoimmune disorders and inflammatory
PT   diseases.
XX
PS   Disclosure; Fig 1; 137pp; English.
XX
CC   The invention relates to novel polypeptides exhibiting a higher
CC   phosphodiesterase 7 (PDE7) catalytic activity than endogenous full length
CC   PDE7 and nucleic acid molecules encoding such polypeptides. Sequences of
CC   the invention are used for screening compounds that inhibit PDE7
CC   activity. PDE7 inhibitors are used for manufacturing a pharmaceutical
CC   composition useful for the treatment or prevention of various
CC   pathological conditions such as diseases affecting the immune system,
CC   including acquired immune deficiency syndrome (AIDS), rejection of
CC   transplant, autoimmune disorders such as T-cells related diseases for
CC   e.g. rheumatoid arthritis, inflammatory diseases such as respiratory
CC   inflammation diseases including chronic obstructive pulmonary disease
CC   (COPD), asthma, gastrointestinal inflammation diseases such as Crohn's
CC   disease, colitis, pancreatitis and different types of cancers including
CC   leukaemia. The present sequence is mouse PDE7A2 protein
XX
SQ   Sequence 456 AA;

  Query Match             93.8%;  Score 2105;  DB 5;  Length 456;
  Best Local Similarity   93.7%;  Pred. No. 2.1e-211;
  Matches  399;  Conservative   13;  Mismatches   14;  Indels    0;  Gaps    0;

Qy          1 DQTALYIRMLGDVRVRSRAGFESERRGSHPYIDFRIFHSQSEIEVSVSARNIRRLLSFQR 60
              |||||||||||||||||||||:||||||||||||||||:|| ||||||||||||||
Db         31 DQTALYIRMLGDVRVRSRAGFETERRGSHPYIDFRIFHSQSDIEASVSARNIRRLLSFQR 90

Qy         61 YLRSSRFFRGTAVSNSLNILDDDYNGQAKCMLEKVGNWNFDIFLFDRLTNGNSLVSLTFH 120
              |||||| |||   | :||:|||:||||||||||||||||||||||||||||||||||||
Db         91 YLRSSRVFRGATVCSSLDILDEDYNGQAKCMLEKVGNWNFDIFLFDRLTNGNSLVSLTFH 150

Qy        121 LFSLHGLIEYFHLDMMKLRRFLVMIQEDYHSQNPYHNAVHAADVTQAMHCYLKEPKLANS 180
              |||||||||||||:|||||||||||||||||||||||||||||||||||||||||||||:|
Db        151 LFSLHGLIEYFHLDMVKLRRFLVMIQEDYHSQNPYHNAVHAADVTQAMHCYLKEPKLASS 210

Qy        181 VTPWDILLSLIAAATHDLDHPGVNQPFLIKTNHYLATLYKNTSVLENHHWRSAVGLLRES 240
              |||||||||||||||||||||||||||||||||||||||||:||||||||||||||||||
Db        211 VTPWDILLSLIAAATHDLDHPGVNQPFLIKTNHYLATLYKNSSVLENHHWRSAVGLLRES 270

Qy        241 GLFSHLPLESRQQMETQIGALILATDISRQNEYLSLFRSHLDRGDLCLEDTRHRHLVLQM 300
              |||||||||||:|| ||||||||||||||||||||||:||| |:| ||||||||
Db        271 GLFSHLPLESRQEMEAQIGALILATDISRQNEYLSLFRSHLDKGDLHLDDGRHRHLVLQM 330

Qy        301 ALKCADICNPCRTWELSKQWSEKVTEEFFHQGDIEKKYHLGVSPLCDRHTESIANIQIGF 360
              |||||||||||| ||||||||||||||||||||||||||||||| ||||||||||
Db        331 ALKCADICNPCRNWELSKQWSEKVTEEFFHQGDIEKKYHLGVSPLCDRQTESIANIQIGF 390

Qy        361 MTYLVEPLFTEWARFSNTRLSQTMLGHVGLNKASWKGLQREQSSSEDTDAAFELNSQLLP 420
              |||||||||||||| ||||||||||||||||||||:| |||| :||||||||||
Db        391 MTYLVEPLFTEWARFSATRLSQTMLGHVGLNKASWKGLQRQQPSSEDANAAFELNSQLLT 450

Qy        421 QENRLS 426
              ||||||
Db        451 QENRLS 456


RESULT 11
AAU79727
ID   AAU79727 standard; protein; 424 AA.
XX
AC   AAU79727;
XX
DT   15-JUL-2002  (first entry)
XX
DE   Human cyclic nucleotide phosphodiesterase, PDE8A variant #3.
XX
KW   Human; cyclic nucleotide phosphodiesterase; PDE; T-cell activation;
KW   immune disorder; graft versus host disease; GVHD; T-cell lymphoma;
KW   acute lymphoblastic leukaemia; autoimmune disease; arthritis;
KW   insulin dependent diabetes mellitus; Crohn's disease; multiple sclerosis;
KW   scleroderma; mixed connective tissue disease; PDE8A; enzyme; variant.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Misc-difference 417
FT                   /label= Unknown
FT                   /note= "Encoded by CAT. This residue is illegible in the
FT                   specification"
XX
PN   WO200222661-A2.
XX
PD   21-MAR-2002.
XX
PF   12-SEP-2001; 2001WO-US028503.
XX
PR   12-SEP-2000; 2000US-0232445P.
PR   12-OCT-2000; 2000US-0240500P.
XX
PA   (BEAV/) BEAVO J A.
PA   (SEEB/) SEEBECK T.
PA   (SODE/) SODERLING S H.
PA   (RASC/) RASCON A.
PA   (ZORA/) ZORAGHI R.
PA   (KUNZ/) KUNZ S.
PA   (GONG/) GONG K.
PA   (GLAV/) GLAVAS N.
XX
PI   Beavo JA,  Seebeck T,  Soderling SH,  Rascon A,  Zoraghi R,  Kunz S;
PI   Gong K,  Glavas N;
XX
DR   WPI; 2002-339862/37.
DR   N-PSDB; ABK48863.
XX
PT   New cyclic nucleotide phosphodiesterase polypeptides such as PDE8A,
PT   PDE7A3, TbPDE2A, TbPDE2B, TbPDE2C or TbPDE2E, that are involved in T cell
PT   activation, useful for diagnosis and treatment of immune disorders.
XX
PS   Example 9; Fig 35; 165pp; English.
XX
CC   The present invention relates to the isolation of novel cyclic nucleotide
CC   phosphodiesterase (PDE) proteins such as PDE8A, PDE7A3, TbPDE2A, TbPDE2B,
CC   TbPDE2C or TbPDE2E, that are involved in T-cell activation or that are
CC   from Trypanosoma brucei. An antibody that recognises a PDE is useful for
CC   isolating a PDE protein from T-cells or a cultured T-cell line. A
CC   molecule that recognises and binds PDE8A or PDE7A3M1 is useful for
CC   inhibiting functional PDE8A- or PDE7A3-associated T-cell interaction, and
CC   for inhibiting an immune system disease. PDE proteins and the
CC   polynucleotide sequences encoding them are useful in the diagnosis and
CC   treatment of immune disorders such as graft versus host disease (GVHD),
CC   psoriasis, immune disorders associated with graft transplantation
CC   rejection, T-cell lymphoma, T- cell acute lymphoblastic leukaemia, and
CC   autoimmune diseases such as Hashimoto's thyroiditis, primary myxoedema,
CC   Grave's disease, insulin dependent diabetes mellitus, pemphigus, Crohn's
CC   disease, multiple sclerosis, ulcerative colitis, Sjogren's syndrome,
CC   arthritis, scleroderma, and mixed connective tissue disease. The present
CC   sequence represents human PDE8A variant #3
XX
SQ   Sequence 424 AA;

  Query Match             85.2%;  Score 1910;  DB 5;  Length 424;
  Best Local Similarity   99.5%;  Pred. No. 5.3e-191;
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  Matches  362;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 DQTALYIRMLGDVRVRSRAGFESERRGSHPYIDFRIFHSQSEIEVSVSARNIRRLLSFQR 60
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Db         57 DQTALYIRMLGDVRVRSRAGFESERRGSHPYIDFRIFHSQSEIEVSVSARNIRRLLSFQR 116

Qy         61 YLRSSRFFRGTAVSNSLNILDDDYNGQAKCMLEKVGNWNFDIFLFDRLTNGNSLVSLTFH 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        117 YLRSSRFFRGTAVSNSLNILDDDYNGQAKCMLEKVGNWNFDIFLFDRLTNGNSLVSLTFH 176

Qy        121 LFSLHGLIEYFHLDMMKLRRFLVMIQEDYHSQNPYHNAVHAADVTQAMHCYLKEPKLANS 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        177 LFSLHGLIEYFHLDMMKLRRFLVMIQEDYHSQNPYHNAVHAADVTQAMHCYLKEPKLANS 236

Qy        181 VTPWDILLSLIAAATHDLDHPGVNQPFLIKTNHYLATLYKNTSVLENHHWRSAVGLLRES 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        237 VTPWDILLSLIAAATHDLDHPGVNQPFLIKTNHYLATLYKNTSVLENHHWRSAVGLLRES 296

Qy        241 GLFSHLPLESRQQMETQIGALILATDISRQNEYLSLFRSHLDRGDLCLEDTRHRHLVLQM 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        297 GLFSHLPLESRQQMETQIGALILATDISRQNEYLSLFRSHLDRGDLCLEDTRHRHLVLQM 356

Qy        301 ALKCADICNPCRTWELSKQWSEKVTEEFFHQGDIEKKYHLGVSPLCDRHTESIANIQIGF 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        357 ALKCADICNPCRTWELSKQWSEKVTEEFFHQGDIEKKYHLGVSPLCDRHTESIANIQIGN 416

Qy        361 MTYL 364
              |||
Db        417 XTYL 420


RESULT 12
AAU16967
ID   AAU16967 standard; protein; 432 AA.
XX
AC   AAU16967;
XX
DT   07-NOV-2001  (first entry)
XX
DE   Human novel secreted protein, SEQ ID 208.
XX
KW   Human; immunosuppressive; antiarthritic; antirheumatic; cytostatic;
KW   cardiant; vasotropic; cerebroprotective; nootropic; neuroprotective;
KW   antibacterial; virucide; fungicide; opthalmalogical; vulnerary;
KW   secreted protein; rheumatoid arthritis; hyperproliferative disorder;
KW   cardiovascular disorder; cardiac arrest; cerebrovascular disorder;
KW   cerebral ischaemia; angiogenesis; nervous system disorder;
KW   Alzheimer's disease; infection; ocular disorder; corneal infection;
KW   wound healing; epithelial cell proliferation; skin ageing; food additive;
KW   preservative; antiproliferative.
XX
OS   Homo sapiens.
XX
PN   WO200155441-A2.
XX
PD   02-AUG-2001.
XX
PF   17-JAN-2001; 2001WO-US001320.
XX
PR   31-JAN-2000; 2000US-0179065P.
PR   04-FEB-2000; 2000US-0180628P.
PR   24-FEB-2000; 2000US-0184664P.
PR   02-MAR-2000; 2000US-0186350P.
PR   16-MAR-2000; 2000US-0189874P.
PR   17-MAR-2000; 2000US-0190076P.
PR   18-APR-2000; 2000US-0198123P.
PR   19-MAY-2000; 2000US-0205515P.
PR   07-JUN-2000; 2000US-0209467P.
PR   28-JUN-2000; 2000US-0214886P.
PR   30-JUN-2000; 2000US-0215135P.
PR   07-JUL-2000; 2000US-0216647P.
PR   07-JUL-2000; 2000US-0216880P.
PR   11-JUL-2000; 2000US-0217487P.
PR   11-JUL-2000; 2000US-0217496P.
PR   14-JUL-2000; 2000US-0218290P.
PR   26-JUL-2000; 2000US-0220963P.
PR   26-JUL-2000; 2000US-0220964P.
PR   14-AUG-2000; 2000US-0224518P.
PR   14-AUG-2000; 2000US-0224519P.
PR   14-AUG-2000; 2000US-0225213P.
PR   14-AUG-2000; 2000US-0225214P.
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PR   14-AUG-2000; 2000US-0225267P.
PR   14-AUG-2000; 2000US-0225268P.
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PR   14-AUG-2000; 2000US-0225447P.
PR   14-AUG-2000; 2000US-0225757P.
PR   14-AUG-2000; 2000US-0225758P.
PR   14-AUG-2000; 2000US-0225759P.
PR   18-AUG-2000; 2000US-0226279P.
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PR   22-AUG-2000; 2000US-0226868P.
PR   22-AUG-2000; 2000US-0227182P.
PR   23-AUG-2000; 2000US-0227009P.
PR   30-AUG-2000; 2000US-0228924P.
PR   01-SEP-2000; 2000US-0229287P.
PR   01-SEP-2000; 2000US-0229343P.
PR   01-SEP-2000; 2000US-0229344P.
PR   01-SEP-2000; 2000US-0229345P.
PR   05-SEP-2000; 2000US-0229509P.
PR   05-SEP-2000; 2000US-0229513P.
PR   06-SEP-2000; 2000US-0230437P.
PR   06-SEP-2000; 2000US-0230438P.
PR   08-SEP-2000; 2000US-0231242P.
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PR   08-SEP-2000; 2000US-0231244P.
PR   08-SEP-2000; 2000US-0231413P.
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PR   08-SEP-2000; 2000US-0232080P.
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PR   12-SEP-2000; 2000US-0231968P.
PR   14-SEP-2000; 2000US-0232397P.
PR   14-SEP-2000; 2000US-0232398P.
PR   14-SEP-2000; 2000US-0232399P.
PR   14-SEP-2000; 2000US-0232400P.
PR   14-SEP-2000; 2000US-0232401P.
PR   14-SEP-2000; 2000US-0233063P.
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PR   21-SEP-2000; 2000US-0234223P.
PR   21-SEP-2000; 2000US-0234274P.
PR   25-SEP-2000; 2000US-0234997P.
PR   25-SEP-2000; 2000US-0234998P.
PR   26-SEP-2000; 2000US-0235484P.
PR   27-SEP-2000; 2000US-0235834P.
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PR   29-SEP-2000; 2000US-0236327P.
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PR   02-OCT-2000; 2000US-0236802P.
PR   02-OCT-2000; 2000US-0237037P.
PR   02-OCT-2000; 2000US-0237038P.
PR   02-OCT-2000; 2000US-0237039P.
PR   02-OCT-2000; 2000US-0237040P.
PR   13-OCT-2000; 2000US-0239935P.
PR   13-OCT-2000; 2000US-0239937P.
PR   20-OCT-2000; 2000US-0240960P.
PR   20-OCT-2000; 2000US-0241221P.
PR   20-OCT-2000; 2000US-0241785P.
PR   20-OCT-2000; 2000US-0241786P.
PR   20-OCT-2000; 2000US-0241787P.
PR   20-OCT-2000; 2000US-0241808P.
PR   20-OCT-2000; 2000US-0241809P.
PR   20-OCT-2000; 2000US-0241826P.
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PR   01-NOV-2000; 2000US-0244617P.
PR   08-NOV-2000; 2000US-0246474P.
PR   08-NOV-2000; 2000US-0246475P.
PR   08-NOV-2000; 2000US-0246476P.
PR   08-NOV-2000; 2000US-0246477P.
PR   08-NOV-2000; 2000US-0246478P.
PR   08-NOV-2000; 2000US-0246523P.
PR   08-NOV-2000; 2000US-0246524P.
PR   08-NOV-2000; 2000US-0246525P.
PR   08-NOV-2000; 2000US-0246526P.
PR   08-NOV-2000; 2000US-0246527P.
PR   08-NOV-2000; 2000US-0246528P.
PR   08-NOV-2000; 2000US-0246532P.
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PR   08-NOV-2000; 2000US-0246610P.
PR   08-NOV-2000; 2000US-0246611P.
PR   08-NOV-2000; 2000US-0246613P.
PR   17-NOV-2000; 2000US-0249207P.
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PR   17-NOV-2000; 2000US-0249209P.
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PR   17-NOV-2000; 2000US-0249215P.
PR   17-NOV-2000; 2000US-0249216P.
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PR   17-NOV-2000; 2000US-0249264P.
PR   17-NOV-2000; 2000US-0249265P.
PR   17-NOV-2000; 2000US-0249297P.
PR   17-NOV-2000; 2000US-0249299P.
PR   17-NOV-2000; 2000US-0249300P.
PR   01-DEC-2000; 2000US-0250160P.
PR   01-DEC-2000; 2000US-0250391P.
PR   05-DEC-2000; 2000US-0251030P.
PR   05-DEC-2000; 2000US-0251988P.
PR   05-DEC-2000; 2000US-0256719P.
PR   06-DEC-2000; 2000US-0251479P.
PR   08-DEC-2000; 2000US-0251856P.
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PR   08-DEC-2000; 2000US-0251869P.
PR   08-DEC-2000; 2000US-0251989P.
PR   08-DEC-2000; 2000US-0251990P.
PR   11-DEC-2000; 2000US-0254097P.
PR   05-JAN-2001; 2001US-0259678P.
XX
PA   (HUMA-) HUMAN GENOME SCI INC.
XX
PI   Rosen CA,  Barash SC,  Ruben SM;
XX
DR   WPI; 2001-476222/51.
DR   N-PSDB; AAS26872.
XX
PT   Novel polypeptides and polynucleotides useful as diagnostic reagents to
PT   diagnose diseases or disorders associated with aberrant expression or
PT   activity of polypeptides, for treating blood clotting disorder,
PT   hemophilia.
XX
PS   Claim 11; SEQ ID NO 208; 601pp; English.
XX
CC   The invention relates to isolated nucleic acid molecules and their
CC   encoded secreted proteins. The nucleic acids and proteins are used to
CC   prevent, treat or ameliorate a medical condition in e.g. humans, mice,
CC   rabbits, goats, horses, cats, dogs, chickens or sheep. They are also used
CC   in diagnosing a pathological condition or susceptibility to a
CC   pathological condition. Antibodies to the proteins can also be used in
CC   alleviating symptoms associated with the disorders and in diagnostic
CC   immunoassays e.g. radioimmunoassays or enzyme linked immunosorbant assays
CC   (ELISA). Disorders which are diagnosed or treated include autoimmune
CC   diseases e.g. rheumatoid arthritis, hyperproliferative disorders e.g.
CC   neoplasms of the breast or liver, cardiovascular disorders e.g. cardiac
CC   arrest, cerebrovascular disorders e.g. cerebral ischaemia, angiogenesis,
CC   nervous system disorders e.g. Alzheimer's disease, infections caused by
CC   bacteria, viruses and fungi and ocular disorders e.g. corneal infection,
CC   and many other disorders listed in the specification. The polypeptides
CC   can also be used to aid wound healing and epithelial cell proliferation,
CC   to prevent skin aging due to sunburn, to maintain organs before
CC   transplantation, for supporting cell culture of primary tissues, to
CC   regenerate tissues and in chemotaxis. The polypeptides can also be used
CC   as a food additive or preservative to increase or decrease storage
CC   capabilities, fat content, lipid, protein, carbohydrate, vitamins,
CC   minerals, cofactors and other nutritional components. The present
CC   sequence represents a novel secreted protein of the invention. Note: The

  Query Match             84.8%;  Score 1903;  DB 4;  Length 432;
  Best Local Similarity   99.2%;  Pred. No. 3e-190;
  Matches  361;  Conservative    0;  Mismatches    3;  Indels    0;  Gaps    0;

Qy          1 DQTALYIRMLGDVRVRSRAGFESERRGSHPYIDFRIFHSQSEIEVSVSARNIRRLLSFQR 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         65 DQTALYIRMLGDVRVRSRAGFESERRGSHPYIDFRIFHSQSEIEVSVSARNIRRLLSFQR 124

Qy         61 YLRSSRFFRGTAVSNSLNILDDDYNGQAKCMLEKVGNWNFDIFLFDRLTNGNSLVSLTFH 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        125 YLRSSRFFRGTAVSNSLNILDDDYNGQAKCMLEKVGNWNFDIFLFDRLTNGNSLVSLTFH 184

Qy        121 LFSLHGLIEYFHLDMMKLRRFLVMIQEDYHSQNPYHNAVHAADVTQAMHCYLKEPKLANS 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        185 LFSLHGLIEYFHLDMMKLRRFLVMIQEDYHSQNPYHNAVHAADVTQAMHCYLKEPKLANS 244

Qy        181 VTPWDILLSLIAAATHDLDHPGVNQPFLIKTNHYLATLYKNTSVLENHHWRSAVGLLRES 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        245 VTPWDILLSLIAAATHDLDHPGVNQPFLIKTNHYLATLYKNTSVLENHHWRSAVGLLRES 304

Qy        241 GLFSHLPLESRQQMETQIGALILATDISRQNEYLSLFRSHLDRGDLCLEDTRHRHLVLQM 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        305 GLFSHLPLESRQQMETQIGALILATDISRQNEYLSLFRSHLDRGDLCLEDTRHRHLVLQM 364

Qy        301 ALKCADICNPCRTWELSKQWSEKVTEEFFHQGDIEKKYHLGVSPLCDRHTESIANIQIGF 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||| ||||
Db        365 ALKCADICNPCRTWELSKQWSEKVTEEFFHQGDIEKKYHLGVSPLCDRHTESIAXIQIGN 424

Qy        361 MTYL 364
                |||
Db        425 YTYL 428


RESULT 13
ABB07912
ID   ABB07912 standard; protein; 336 AA.
XX
AC   ABB07912;
XX
DT   30-JUL-2002  (first entry)
XX
DE   Human PDE7a3 splice variant polypeptide.
XX
KW   Cyclic adenosine monophosphate; cAMP; cAMP phosphodiesterase type 7;
KW   PDE7a3; splice variant; transgenic; cardiant; antiinflammatory;
KW   antiallergic; antiasthmatic; antiinfertility; vaccine; enzyme.
XX
OS   Homo sapiens.
XX
PN   WO200183772-A1.
XX
PD   08-NOV-2001.
XX
PF   27-APR-2001; 2001WO-EP004785.
XX
PR   28-APR-2000; 2000EP-00109267.
XX
PA   (MERE ) MERCK PATENT GMBH.
```

XX
PI Kluxen F;
XX
DR WPI; 2002-034516/04.
DR N-PSDB; ABL58391.
XX
PT New polypeptide of splice variant of cyclic adenosine monophosphate
PT phosphodiesterase type 7 and polynucleotides, useful as vaccines for
PT inducing immune response against diseases e.g. cardiovascular diseases
PT and asthma.
XX
PS Claim 2; Page 33-36; 40pp; English.
XX
CC This represents a splice variant of cyclic adenosine monophosphate (cAMP)
CC phosphodiesterase type 7 (PDE7a3). The polypeptide can be expressed by
CC standard recombinant methodology. The PDE7a3 splice variant polypeptides
CC and polynucleotides are useful for treating cardiovascular diseases,
CC asthma, allergy, inflammatory diseases, fertility disorders and
CC immunoregulator disorders. The polynucleotides are useful for producing
CC transgenic animals, which include knock-in animals (in which an animal
CC gene is replaced by human equivalent within the genome of the animal),
CC useful in drug discovery process, for target validation. The PDE7a3
CC splice variant polypeptides and polynucleotides are useful as vaccines
CC for inducing an immunological response in a mammal
XX
SQ Sequence 336 AA;

Query Match 79.7%; Score 1787; DB 5; Length 336;
Best Local Similarity 100.0%; Pred. No. 3e-178;
Matches 336; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          91 MLEKVGNWNFDIFLFDRLTNGNSLVSLTFHLFSLHGLIEYFHLDMMKLRRFLVMIQEDYH 150
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db           1 MLEKVGNWNFDIFLFDRLTNGNSLVSLTFHLFSLHGLIEYFHLDMMKLRRFLVMIQEDYH 60

Qy         151 SQNPYHNAVHAADVTQAMHCYLKEPKLANSVTPWDILLSLIAAATHDLDHPGVNQPFLIK 210
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          61 SQNPYHNAVHAADVTQAMHCYLKEPKLANSVTPWDILLSLIAAATHDLDHPGVNQPFLIK 120

Qy         211 TNHYLATLYKNTSVLENHHWRSAVGLLRESGLFSHLPLESRQQMETQIGALILATDISRQ 270
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         121 TNHYLATLYKNTSVLENHHWRSAVGLLRESGLFSHLPLESRQQMETQIGALILATDISRQ 180

Qy         271 NEYLSLFRSHLDRGDLCLEDTRHRHLVLQMALKCADICNPCRTWELSKQWSEKVTEEFFH 330
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         181 NEYLSLFRSHLDRGDLCLEDTRHRHLVLQMALKCADICNPCRTWELSKQWSEKVTEEFFH 240

Qy         331 QGDIEKKYHLGVSPLCDRHTESIANIQIGFMTYLVEPLFTEWARFSNTRLSQTMLGHVGL 390
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         241 QGDIEKKYHLGVSPLCDRHTESIANIQIGFMTYLVEPLFTEWARFSNTRLSQTMLGHVGL 300

Qy         391 NKASWKGLQREQSSSEDTDAAFELNSQLLPQENRLS 426
               |||||||||||||||||||||||||||||||||||
Db         301 NKASWKGLQREQSSSEDTDAAFELNSQLLPQENRLS 336
```

RESULT 14
AAU79713
ID AAU79713 standard; protein; 424 AA.
XX
AC AAU79713;
XX
DT 15-JUL-2002 (first entry)
XX
DE Human phosphodiesterase, PDE7A3 splice variant.
XX
KW Human; cyclic nucleotide phosphodiesterase; PDE; T-cell activation;
KW immune disorder; graft versus host disease; GVHD; T-cell lymphoma;
KW acute lymphoblastic leukaemia; autoimmune disease; arthritis;
KW insulin dependent diabetes mellitus; Crohn's disease; multiple sclerosis;
KW scleroderma; mixed connective tissue disease; PDE7A3; enzyme; variant.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT misc_feature 1. .424
FT /label= Unknown
FT /note= "All residues represented by Xaa are illegible in
FT the specification"
XX
PN WO200222661-A2.
XX
PD 21-MAR-2002.
XX
PF 12-SEP-2001; 2001WO-US028503.
XX
PR 12-SEP-2000; 2000US-0232445P.
PR 12-OCT-2000; 2000US-0240500P.
XX
PA (BEAV/) BEAVO J A.
PA (SEEB/) SEEBECK T.
PA (SODE/) SODERLING S H.
PA (RASC/) RASCON A.
PA (ZORA/) ZORAGHI R.
PA (KUNZ/) KUNZ S.
PA (GONG/) GONG K.
PA (GLAV/) GLAVAS N.
XX
PI Beavo JA, Seebeck T, Soderling SH, Rascon A, Zoraghi R, Kunz S;
PI Gong K, Glavas N;
XX
DR WPI; 2002-339862/37.
XX
PT New cyclic nucleotide phosphodiesterase polypeptides such as PDE8A,
PT PDE7A3, TbPDE2A, TbPDE2B, TbPDE2C or TbPDE2E, that are involved in T cell
PT activation, useful for diagnosis and treatment of immune disorders.
XX
PS Claim 2; Fig 8B; 165pp; English.
XX
CC The present invention relates to the isolation of novel cyclic nucleotide
CC phosphodiesterase (PDE) proteins such as PDE8A, PDE7A3, TbPDE2A, TbPDE2B,
CC TbPDE2C or TbPDE2E, that are involved in T-cell activation or that are
CC from Trypanosoma brucei. An antibody that recognises a PDE is useful for
CC isolating a PDE protein from T-cells or a cultured T-cell line. A
CC molecule that recognises and binds PDE8A or PDE7A3M1 is useful for
CC inhibiting functional PDE8A- or PDE7A3-associated T-cell interaction, and
CC for inhibiting an immune system disease. PDE proteins and the
CC polynucleotide sequences encoding them are useful in the diagnosis and
CC treatment of immune disorders such as graft versus host disease (GVHD),
CC psoriasis, immune disorders associated with graft transplantation
CC rejection, T-cell lymphoma, T- cell acute lymphoblastic leukaemia, and
CC autoimmune diseases such as Hashimoto's thyroiditis, primary myxoedema,
CC Grave's disease, insulin dependent diabetes mellitus, pemphigus, Crohn's
CC disease, multiple sclerosis, ulcerative colitis, Sjogren's syndrome,
CC arthritis, scleroderma, and mixed connective tissue disease. The present
CC sequence represents human PDE7A3 splice variant. Note: The present
CC sequence should be encoded by ABK48831. However, since the present
CC sequence is of poor quality in the specification many of the residues are
CC illegible
XX
SQ Sequence 424 AA;

Query Match 76.5%; Score 1717; DB 5; Length 424;
Best Local Similarity 92.0%; Pred. No. 9.4e-171;
Matches 335; Conservative 0; Mismatches 29; Indels 0; Gaps 0;

```
Qy           1 DQTALYIRMLGDVRVRSRAGFESERRGSHPYIDFRIFHSQSEIEVSVSARNIRRLLSFQR 60
               |||||| |||||| |||||||||||||| |||||||||||||||||||||||||| ||| |
Db          57 DQTALYXRMLGDVXVRSRAGFESERRGSXXYIDFRIFHSQSEIEVSVSARNIRRLLXFQR 116

Qy          61 YLRSSRFFRGTAVSNSLNILDDDYNGQAKCMLEKVGNWNFDIFLFDRLTNGNSLVSLTFH 120
               ||||||| ||||||||||||||||||||||||||||   ||||||||||||||||||||||
Db         117 YLRSSRFXRGTAVSNSLNILDDDYNGQAKCMLEKVGXXXFDIFLFDRLTNGNSLVSLTFH 176

Qy         121 LFSLHGLIEYFHLDMMKLRRFLVMIQEDYHSQNPYHNAVHAADVTQAMHCYLKEPKLANS 180
               | |||||||||||||||||||||||||||||||||| ||||||||| ||| ||||| ||
```

```
Db        177 LXSLHGLIEYFHLDMMKLRRFLVMIQEDYHSQNPYHXAVHAADVTQAXHCYXKEPKLXNS 236

Qy        181 VTPWDILLSLIAAATHDLDHPGVNQPFLIKTNHYLATLYKNTSVLENHHWRSAVGLLRES 240

Db        237 VXXXDILLSLIAAATHDLDHPGVNQPFLIKTNHYLATLYKNTSVLENXXWRSAVGLLRES 296

Qy        241 GLFSHLPLESRQQMETQIGALILATDISRQNEYLSLFRSHLDRGDLCLEDTRHRHLVLQM 300

Db        297 GLFSHLPXEXRQQMETQIGALILATDISRQNEYLSLFRSHXDRGDLCLEDTRHRHLVLQM 356

Qy        301 ALKCADICNPCRTWELSKQWSEKVTEEFFHQGDIEKKYHLGVSPLCDRHTESIANIQIGF 360

Db        357 ALKCADICNPCRXWELSKQXSEKVTEEFFHQGDIEXKYHLGVSPLCDRXTESIANIQIGN 416

Qy        361 MTYL 364

Db        417 YXYL 420


RESULT 15
AAY93569
ID   AAY93569 standard; protein; 450 AA.
XX
AC   AAY93569;
XX
DT   25-SEP-2000  (first entry)
XX
DE   Amino acid sequence of a human phosphodiesterase enzyme.
XX
KW   Phosphodiesterase; PDE-XIV; human; enzyme.
XX
OS   Homo sapiens.
XX
PN   EP1018559-A1.
XX
PD   12-JUL-2000.
XX
PF   09-NOV-1999;   99EP-00308902.
XX
PR   23-DEC-1998;   98GB-00028603.
PR   17-SEP-1999;   99GB-00022123.
XX
PA   (PFIZ ) PFIZER LTD.
PA   (PFIZ ) PFIZER INC.
XX
PI   Fidock M;
XX
DR   WPI; 2000-433274/38.
DR   N-PSDB; AAA46651.
XX
PT   Nucleic acids encoding recombinant phosphodiesterase (PDE)-XIV enzymes,
PT   useful for preventing diagnosing and treating diseases associated with
PT   inappropriate PDE-XIV expression and/or activity.
XX
PS   Disclosure; Page 45-47; 104pp; English.
XX
CC   The present sequence represents a phosphodiesterase (PDE)-XIV enzyme. The
CC   phosphodiesterase polynucleotide and polypeptide may be used in the
CC   prevention, treatment and diagnosis of diseases associated with
CC   inappropriate PDE-XIV expression. For example, the polynucleotide be
CC   administered to treat diseases by rectifying mutations or deletions in a
CC   patient's genome that affect the activity of PDE-XIV. They may also be
CC   used to study the expression and function of PDE-XIV polypeptides and
CC   their role in metabolism. The PDE-XIV polypeptides may be used as
CC   antigens in the production of antibodies against PDE-XIV and in assays to
CC   identify modulators (agonists and antagonists) of PDE-XIV expression and
CC   activity. The anti-PDE-XIV antibodies and PDE-XIV antagonists may also be
CC   used to down regulate PDE-XIV expression and activity (i.e. the PDE-XIV
CC   gene and/or expression product may be used in the preparation of a
CC   composition for the treatment of a disorder associated with inappropriate
CC   PDE-XIV expression and/or activity and to screen for agents that can
CC   modulate PDE-XIV expression and or activity. The anti-PDE-XIV antibodies
CC   may also be used as diagnostic agents for detecting the presence of PDE-
CC   XIV polypeptides in samples (e.g. by enzyme linked immunosorbant assay
CC   (ELISA))
XX
SQ   Sequence 450 AA;

  Query Match             62.6%;  Score 1403.5;  DB 3;  Length 450;
  Best Local Similarity   62.6%;  Pred. No. 7.9e-138;
  Matches  258;  Conservative   66;  Mismatches   87;  Indels    1;  Gaps    1;

Qy          1 DQTALYIRMLGDVRVRSRAGFESERRGSHPYIDFRIFHSQSEIEVSVSARNIRRLLSFQR 60

Db         18 DQNAKCVCMLGDIRLRGQTGVRAERRGSYPFIDFRLLNSTTYSGEIGTKKKVKRLLSFQR 77

Qy         61 YLRSSRFFRGTAVSNSLNILDDDYNGQAKCMLEKVGNWNFDIFLFDRLTNGNSLVSLTFH 120

Db         78 YFHASRLLRGIIPQAPLHLLDEDYLGQARHMLSKVGMWDFDIFLFDRLTNGNSLVTLLCH 137

Qy        121 LFSLHGLIEYFHLDMMKLRRFLVMIQEDYHSQNPYHNAVHAADVTQAMHCYLKEPKLANS 180

Db        138 LFNTHGLIHHFKLDMVTLHRFLVMVQEDYHSQNPYHNAVHAADVTQAMHCYLKEPKLASF 197

Qy        181 VTPWDILLSLIAAATHDLDHPGVNQPFLIKTNHYLATLYKNTSVLENHHWRSAVGLLRES 240

Db        198 LTPLDIMLGLLAAAAHDVDHPGVNQPFLIKTNHHLANLYQNMSVLENHHWRSTIGMLRES 257

Qy        241 GLFSHLPLESRQQMETQIGALILATDISRQNEYLSLFRSHLDRGDLCLEDTRHRHLVLQM 300

Db        258 RLLAHLPKEMTQDIEQQLGSLILATDINRQNEFLTRLKAHLHNKDLRLEDAQDRHFMLQI 317

Qy        301 ALKCADICNPCRTWELSKQWSEKVTEEFFHQGDIEKKYHLGVSPLCDRHTESIANIQIGF 360

Db        318 ALKCADICNPCRIWEMSKQWSERVCEEFYRQGELEQKFELEISPLCNQQKDSIPSIQIGF 377

Qy        361 MTYLVEPLFTEWARFS-NTRLSQTMLGHVGLNKASWKGLQREQSSSEDTDAA 411

Db        378 MSYIVEPLFREWAHFTGNSTLSENMLGHLAHNKAQWKSLLPRQHRSRGSSGS 429


Search completed: May 26, 2004, 09:28:27
Job time : 99 secs
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GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: May 26, 2004, 09:24:28 ; Search time 23 Seconds
(without alignments)
956.203 Million cell updates/sec

Title: US-09-966-781A-1
Perfect score: 2243
Sequence: 1 DQTALYIRMLGDVRVRSRAG.....DTDAAFELNSQLLPQENRLS 426

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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1: /cgn2_6/ptodata/2/iaa/5A_COMB.pep:*
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3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/2/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	2243	100.0	498	1	US-07-688-352C-20	Sequence 20, Appl
2	2243	100.0	498	2	US-08-474-379C-20	Sequence 20, Appl
3	2243	100.0	498	3	US-09-146-249A-20	Sequence 20, Appl
4	2243	100.0	498	3	US-08-206-188B-20	Sequence 20, Appl
5	1383.5	61.7	502	3	US-09-330-970-1	Sequence 1, Appli
6	871	38.8	320	3	US-09-330-970-3	Sequence 3, Appli
7	555	24.7	610	2	US-08-974-565C-9	Sequence 9, Appli
8	555	24.7	610	3	US-09-255-748-9	Sequence 9, Appli
9	550	24.5	562	1	US-07-688-352C-4	Sequence 4, Appli
10	550	24.5	562	2	US-08-942-521B-8	Sequence 8, Appli
11	550	24.5	562	2	US-08-474-379C-4	Sequence 4, Appli
12	550	24.5	562	3	US-09-146-249A-4	Sequence 4, Appli
13	550	24.5	562	3	US-08-206-188B-4	Sequence 4, Appli
14	550	24.5	562	5	PCT-US91-02714-4	Sequence 4, Appli
15	550	24.5	564	2	US-08-942-521B-2	Sequence 2, Appli
16	550	24.5	564	2	US-08-474-379C-59	Sequence 59, Appl
17	550	24.5	564	3	US-09-146-249A-59	Sequence 59, Appl
18	550	24.5	564	3	US-08-206-188B-59	Sequence 59, Appl
19	550	24.5	564	3	US-09-192-702-2	Sequence 2, Appli
20	550	24.5	564	4	US-08-445-474-2	Sequence 2, Appli
21	550	24.5	564	5	PCT-US94-02612-2	Sequence 2, Appli
22	550	24.5	736	1	US-07-688-352C-24	Sequence 24, Appl
23	550	24.5	736	2	US-08-474-379C-24	Sequence 24, Appl
24	550	24.5	736	3	US-09-146-249A-24	Sequence 24, Appl
25	550	24.5	736	3	US-08-206-188B-24	Sequence 24, Appl
26	550	24.5	736	5	PCT-US91-02714-23	Sequence 23, Appl
27	549	24.5	564	2	US-08-577-492-34	Sequence 34, Appl
28	549	24.5	564	3	US-09-079-630-34	Sequence 34, Appl
29	548.5	24.5	610	2	US-08-942-521B-7	Sequence 7, Appli
30	545	24.3	481	1	US-08-286-856C-2	Sequence 2, Appli
31	545	24.3	481	1	US-08-472-831-2	Sequence 2, Appli
32	545	24.3	506	1	US-08-286-856C-3	Sequence 3, Appli
33	545	24.3	506	1	US-08-472-831-3	Sequence 3, Appli
34	545	24.3	606	2	US-08-577-492-32	Sequence 32, Appl
35	545	24.3	606	3	US-09-079-630-32	Sequence 32, Appl
36	543	24.2	501	2	US-08-577-492-40	Sequence 40, Appl
37	543	24.2	501	3	US-09-079-630-40	Sequence 40, Appl
38	542	24.2	517	4	US-08-472-600-6	Sequence 6, Appli
39	542	24.2	517	4	US-09-717-953-6	Sequence 6, Appli
40	542	24.2	518	4	US-09-602-735B-2	Sequence 2, Appli
41	542	24.2	564	4	US-08-472-600-5	Sequence 5, Appli
42	542	24.2	564	4	US-09-717-953-5	Sequence 5, Appli
43	542	24.2	673	2	US-08-577-492-35	Sequence 35, Appl
44	542	24.2	673	2	US-08-474-379C-63	Sequence 63, Appl
45	542	24.2	673	3	US-09-146-249A-63	Sequence 63, Appl

ALIGNMENTS

```
RESULT 1
US-07-688-352C-20
; Sequence 20, Application US/07688352C
; Patent No. 5527896
;  GENERAL INFORMATION:
;    APPLICANT:  Wigler, Michael H.
;    APPLICANT:  Colicelli, John J.
;    TITLE OF INVENTION:  Cloning by Complementation and Related
;    TITLE OF INVENTION:  Processes
;    NUMBER OF SEQUENCES:  57
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Marshall, O'Toole, Gerstein, Murray &
;      ADDRESSEE:  Bicknell
;      STREET:  Two First National Plaza, 20 South Clark
;      STREET:  Street
;      CITY:  Chicago
;      STATE:  Illinois
;      COUNTRY:  USA
;      ZIP:  60603
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/07/688,352C
;      FILING DATE:  19910419
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/511,715
;      FILING DATE:  20-APR-1990
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Borun, Michael F.
;      REGISTRATION NUMBER:  25447
;      REFERENCE/DOCKET NUMBER:  27805/30197
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (312) 346-5750
;      TELEFAX:  (312) 984-9740
;      TELEX:  25-3856
;  INFORMATION FOR SEQ ID NO:  20:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  498 amino acids
;      TYPE:  AMINO ACID
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-07-688-352C-20

  Query Match           100.0%;  Score 2243;  DB 1;  Length 498;
  Best Local Similarity  100.0%;  Pred. No. 5.4e-232;
  Matches  426;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;
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```
Qy          1 DQTALYIRMLGDVRVRSRAGFESERRGSHPYIDFRIFHSQSEIEVSVSARNIRRLLSFQR 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         73 DQTALYIRMLGDVRVRSRAGFESERRGSHPYIDFRIFHSQSEIEVSVSARNIRRLLSFQR 132

Qy         61 YLRSSRFFRGTAVSNSLNILDDDYNGQAKCMLEKVGNWNFDIFLFDRLTNGNSLVSLTFH 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        133 YLRSSRFFRGTAVSNSLNILDDDYNGQAKCMLEKVGNWNFDIFLFDRLTNGNSLVSLTFH 192

Qy        121 LFSLHGLIEYFHLDMMKLRRFLVMIQEDYHSQNPYHNAVHAADVTQAMHCYLKEPKLANS 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        193 LFSLHGLIEYFHLDMMKLRRFLVMIQEDYHSQNPYHNAVHAADVTQAMHCYLKEPKLANS 252

Qy        181 VTPWDILLSLIAAATHDLDHPGVNQPFLIKTNHYLATLYKNTSVLENHHWRSAVGLLRES 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        253 VTPWDILLSLIAAATHDLDHPGVNQPFLIKTNHYLATLYKNTSVLENHHWRSAVGLLRES 312

Qy        241 GLFSHLPLESRQQMETQIGALILATDISRQNEYLSLFRSHLDRGDLCLEDTRHRHLVLQM 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        313 GLFSHLPLESRQQMETQIGALILATDISRQNEYLSLFRSHLDRGDLCLEDTRHRHLVLQM 372

Qy        301 ALKCADICNPCRTWELSKQWSEKVTEEFFHQGDIEKKYHLGVSPLCDRHTESIANIQIGF 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        373 ALKCADICNPCRTWELSKQWSEKVTEEFFHQGDIEKKYHLGVSPLCDRHTESIANIQIGF 432

Qy        361 MTYLVEPLFTEWARFSNTRLSQTMLGHVGLNKASWKGLQREQSSSEDTDAAFELNSQLLP 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        433 MTYLVEPLFTEWARFSNTRLSQTMLGHVGLNKASWKGLQREQSSSEDTDAAFELNSQLLP 492

Qy        421 QENRLS 426
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Db        493 QENRLS 498
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RESULT 2
US-08-474-379C-20
; Sequence 20, Application US/08474379C
; Patent No. 5977305
;  GENERAL INFORMATION:
;    APPLICANT:  Wigler, Michael H.
;    APPLICANT:  Colicelli, John J.
;    TITLE OF INVENTION:  CLONING BY COMPLEMENTATION AND RELATED
;    TITLE OF INVENTION:  PROCESSES
;    NUMBER OF SEQUENCES:  88
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Marshall, O'Toole, Gerstein, Murray & Borun
;      STREET:  233 South Wacker Drive/6300 Sears Tower
;      CITY:  Chicago
;      STATE:  Illinois
;      COUNTRY:  United States of America
;      ZIP:  60606-6402
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/474,379C
;      FILING DATE:  07-JUN-1995
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/511,715
;      FILING DATE:  20-APR-1990
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/206,188
;      FILING DATE:  01-MAR-1994
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/688,352
;      FILING DATE:  19-APR-1991
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Clough, David W.
;      REGISTRATION NUMBER:  36,107
;      REFERENCE/DOCKET NUMBER:  27866/32771
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (312) 474-6300
;      TELEFAX:  (312) 474-0448
;  INFORMATION FOR SEQ ID NO:  20:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  498 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-474-379C-20

  Query Match             100.0%;  Score 2243;  DB 2;  Length 498;
  Best Local Similarity   100.0%;  Pred. No. 5.4e-232;
  Matches  426;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;
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Qy          1 DQTALYIRMLGDVRVRSRAGFESERRGSHPYIDFRIFHSQSEIEVSVSARNIRRLLSFQR 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         73 DQTALYIRMLGDVRVRSRAGFESERRGSHPYIDFRIFHSQSEIEVSVSARNIRRLLSFQR 132

Qy         61 YLRSSRFFRGTAVSNSLNILDDDYNGQAKCMLEKVGNWNFDIFLFDRLTNGNSLVSLTFH 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        133 YLRSSRFFRGTAVSNSLNILDDDYNGQAKCMLEKVGNWNFDIFLFDRLTNGNSLVSLTFH 192

Qy        121 LFSLHGLIEYFHLDMMKLRRFLVMIQEDYHSQNPYHNAVHAADVTQAMHCYLKEPKLANS 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        193 LFSLHGLIEYFHLDMMKLRRFLVMIQEDYHSQNPYHNAVHAADVTQAMHCYLKEPKLANS 252

Qy        181 VTPWDILLSLIAAATHDLDHPGVNQPFLIKTNHYLATLYKNTSVLENHHWRSAVGLLRES 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        253 VTPWDILLSLIAAATHDLDHPGVNQPFLIKTNHYLATLYKNTSVLENHHWRSAVGLLRES 312

Qy        241 GLFSHLPLESRQQMETQIGALILATDISRQNEYLSLFRSHLDRGDLCLEDTRHRHLVLQM 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        313 GLFSHLPLESRQQMETQIGALILATDISRQNEYLSLFRSHLDRGDLCLEDTRHRHLVLQM 372

Qy        301 ALKCADICNPCRTWELSKQWSEKVTEEFFHQGDIEKKYHLGVSPLCDRHTESIANIQIGF 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        373 ALKCADICNPCRTWELSKQWSEKVTEEFFHQGDIEKKYHLGVSPLCDRHTESIANIQIGF 432

Qy        361 MTYLVEPLFTEWARFSNTRLSQTMLGHVGLNKASWKGLQREQSSSEDTDAAFELNSQLLP 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        433 MTYLVEPLFTEWARFSNTRLSQTMLGHVGLNKASWKGLQREQSSSEDTDAAFELNSQLLP 492

Qy        421 QENRLS 426
              ||||||
Db        493 QENRLS 498
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RESULT 3
US-09-146-249A-20
; Sequence 20, Application US/09146249A
; Patent No. 6069240
;  GENERAL INFORMATION:
;    APPLICANT:  Wigler, Michael H.
;    APPLICANT:  Colicelli, John J.
;    TITLE OF INVENTION:  Cloning by Complementation and Related
;    TITLE OF INVENTION:  Processes
;    NUMBER OF SEQUENCES:  85
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Marshall, O'Toole, Gerstein, Murray & Borun
;      STREET:  6300 Sears Tower, 233 South Wacker Drive
;      CITY:  Chicago
;      STATE:  Illinois
;      COUNTRY:  United States of America
;      ZIP:  60606-6402
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/146,249A
;      FILING DATE:
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;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/511,715
;      FILING DATE:  20-APR-1990
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Clough, David W.
;      REGISTRATION NUMBER:  36,107
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  312/474-6300
;      TELEFAX:  312-474-0448
;      TELEX:  25-3856
;  INFORMATION FOR SEQ ID NO:  20:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  498 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-09-146-249A-20

  Query Match           100.0%;  Score 2243;  DB 3;  Length 498;
  Best Local Similarity  100.0%;  Pred. No. 5.4e-232;
  Matches  426;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 DQTALYIRMLGDVRVRSRAGFESERRGSHPYIDFRIFHSQSEIEVSVSARNIRRLLSFQR 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         73 DQTALYIRMLGDVRVRSRAGFESERRGSHPYIDFRIFHSQSEIEVSVSARNIRRLLSFQR 132

Qy         61 YLRSSRFFRGTAVSNSLNILDDDYNGQAKCMLEKVGNWNFDIFLFDRLTNGNSLVSLTFH 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        133 YLRSSRFFRGTAVSNSLNILDDDYNGQAKCMLEKVGNWNFDIFLFDRLTNGNSLVSLTFH 192

Qy        121 LFSLHGLIEYFHLDMMKLRRFLVMIQEDYHSQNPYHNAVHAADVTQAMHCYLKEPKLANS 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        193 LFSLHGLIEYFHLDMMKLRRFLVMIQEDYHSQNPYHNAVHAADVTQAMHCYLKEPKLANS 252

Qy        181 VTPWDILLSLIAAATHDLDHPGVNQPFLIKTNHYLATLYKNTSVLENHHWRSAVGLLRES 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        253 VTPWDILLSLIAAATHDLDHPGVNQPFLIKTNHYLATLYKNTSVLENHHWRSAVGLLRES 312

Qy        241 GLFSHLPLESRQQMETQIGALILATDISRQNEYLSLFRSHLDRGDLCLEDTRHRHLVLQM 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        313 GLFSHLPLESRQQMETQIGALILATDISRQNEYLSLFRSHLDRGDLCLEDTRHRHLVLQM 372

Qy        301 ALKCADICNPCRTWELSKQWSEKVTEEFFHQGDIEKKYHLGVSPLCDRHTESIANIQIGF 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        373 ALKCADICNPCRTWELSKQWSEKVTEEFFHQGDIEKKYHLGVSPLCDRHTESIANIQIGF 432

Qy        361 MTYLVEPLFTEWARFSNTRLSQTMLGHVGLNKASWKGLQREQSSSEDTDAAFELNSQLLP 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        433 MTYLVEPLFTEWARFSNTRLSQTMLGHVGLNKASWKGLQREQSSSEDTDAAFELNSQLLP 492

Qy        421 QENRLS 426
              ||||||
Db        493 QENRLS 498


RESULT 4
US-08-206-188B-20
; Sequence 20, Application US/08206188B
; Patent No. 6100025
;  GENERAL INFORMATION:
;    APPLICANT:  Wigler, Michael H.
;    APPLICANT:  Colicelli, John J.
;    TITLE OF INVENTION:  Cloning by Complementation and Related
;    TITLE OF INVENTION:  Processes
;    NUMBER OF SEQUENCES:  84
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Marshall, O'Toole, Gerstein, Murray & Borun
;      STREET:  6300 Sears Tower, 233 South Wacker Drive
;      CITY:  Chicago
;      STATE:  Illinois
;      COUNTRY:  United States of America
;      ZIP:  60606-6402
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/206,188B
;      FILING DATE:  01-MAR-1994
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/511,715
;      FILING DATE:  20-APR-1990
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Clough, David W.
;      REGISTRATION NUMBER:  36107
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  312/474-6300
;      TELEFAX:  312-474-0448
;      TELEX:  25-3856
;  INFORMATION FOR SEQ ID NO:  20:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  498 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-206-188B-20

  Query Match           100.0%;  Score 2243;  DB 3;  Length 498;
  Best Local Similarity  100.0%;  Pred. No. 5.4e-232;
  Matches  426;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 DQTALYIRMLGDVRVRSRAGFESERRGSHPYIDFRIFHSQSEIEVSVSARNIRRLLSFQR 60
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Db         73 DQTALYIRMLGDVRVRSRAGFESERRGSHPYIDFRIFHSQSEIEVSVSARNIRRLLSFQR 132

Qy         61 YLRSSRFFRGTAVSNSLNILDDDYNGQAKCMLEKVGNWNFDIFLFDRLTNGNSLVSLTFH 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        133 YLRSSRFFRGTAVSNSLNILDDDYNGQAKCMLEKVGNWNFDIFLFDRLTNGNSLVSLTFH 192

Qy        121 LFSLHGLIEYFHLDMMKLRRFLVMIQEDYHSQNPYHNAVHAADVTQAMHCYLKEPKLANS 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        193 LFSLHGLIEYFHLDMMKLRRFLVMIQEDYHSQNPYHNAVHAADVTQAMHCYLKEPKLANS 252

Qy        181 VTPWDILLSLIAAATHDLDHPGVNQPFLIKTNHYLATLYKNTSVLENHHWRSAVGLLRES 240
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Db        253 VTPWDILLSLIAAATHDLDHPGVNQPFLIKTNHYLATLYKNTSVLENHHWRSAVGLLRES 312

Qy        241 GLFSHLPLESRQQMETQIGALILATDISRQNEYLSLFRSHLDRGDLCLEDTRHRHLVLQM 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        313 GLFSHLPLESRQQMETQIGALILATDISRQNEYLSLFRSHLDRGDLCLEDTRHRHLVLQM 372

Qy        301 ALKCADICNPCRTWELSKQWSEKVTEEFFHQGDIEKKYHLGVSPLCDRHTESIANIQIGF 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        373 ALKCADICNPCRTWELSKQWSEKVTEEFFHQGDIEKKYHLGVSPLCDRHTESIANIQIGF 432

Qy        361 MTYLVEPLFTEWARFSNTRLSQTMLGHVGLNKASWKGLQREQSSSEDTDAAFELNSQLLP 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        433 MTYLVEPLFTEWARFSNTRLSQTMLGHVGLNKASWKGLQREQSSSEDTDAAFELNSQLLP 492

Qy        421 QENRLS 426
              ||||||
Db        493 QENRLS 498


RESULT 5
US-09-330-970-1
; Sequence 1, Application US/09330970
; Patent No. 6146876
; GENERAL INFORMATION:
;  APPLICANT: Robison, Keith E.
;  APPLICANT: Kapeller-Libermann, Rosana
```

```
;  APPLICANT: White, David
;  TITLE OF INVENTION: A No. 6146876el Human Cyclic Nucleotide
;  TITLE OF INVENTION: Phophodiesterase
;  FILE REFERENCE: 5800-28
;  CURRENT APPLICATION NUMBER: US/09/330,970
;  CURRENT FILING DATE: 1999-06-11
;  EARLIER APPLICATION NUMBER: 09/277,423
;  EARLIER FILING DATE: 1999-03-26
;  NUMBER OF SEQ ID NOS: 40
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 1
;    LENGTH: 502
;    TYPE: PRT
;    ORGANISM: Homo sapiens
US-09-330-970-1

  Query Match             61.7%;  Score 1383.5;  DB 3;  Length 502;
  Best Local Similarity   62.9%;  Pred. No. 1.1e-139;
  Matches  253;  Conservative   65;  Mismatches   83;  Indels    1;  Gaps    1;

Qy         11 GDVRVRSRAGFESERRGSHPYIDFRIFHSQSEIEVSVSARNIRRLLSFQRYLRSSRFFRG 70
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Db         80 GDIRLRGQTGVRAERRGSYPFIDFRLLNSTTYSGEIGTKKKVKRLLSFQRYFHASRLLRG 139

Qy         71 TAVSNSLNILDDDYNGQAKCMLEKVGNWNFDIFLFDRLTNGNSLVSLTFHLFSLHGLIEY 130
                    |::||:|| |||: || ||| |:||||||||||||||:|  |||: |||| :
Db        140 IIPQAPLHLLDEDYLGQARHMLSKVGMWDFDIFLFDRLTNGNSLVTLLCHLFNTHGLIHH 199

Qy        131 FHLDMMKLRRFLVMIQEDYHSQNPYHNAVHAADVTQAMHCYLKEPKLANSVTPWDILLSL 190
              | |||: | |||||:|||||||||||||||||||||||||||||||: :|| ||:| |
Db        200 FKLDMVTLHRFLVMVQEDYHSQNPYHNAVHAADVTQAMHCYLKEPKLASFLTPLDIMLGL 259

Qy        191 IAAATHDLDHPGVNQPFLIKTNHYLATLYKNTSVLENHHWRSAVGLLRESGLFSHLPLES 250
              :||| ||:|||||||||||||:|| ||:| |||||||||| :|:|||| | :||| |
Db        260 LAAAAHDVDHPGVNQPFLIKTNHHLANLYQNMSVLENHHWRSTIGMLRESRLLAHLPKEM 319

Qy        251 RQQMETQIGALILATDISRQNEYLSLFRSHLDRGDLCLEDTRHRHLVLQMALKCADICNP 310
              | :| |:|:|||||||:||||:|:  ::||   || ||| : || :||:|||||||||
Db        320 TQDIEQQLGSLILATDINRQNEFLTRLKAHLHNKDLRLEDAQDRHFMLQIALKCADICNP 379

Qy        311 CRTWELSKQWSEKVTEEFFHQGDIEKKYHLGVSPLCDRHTESIANIQIGFMTYLVEPLFT 370
              || ||:|||||:| |||: ||::|:|: | :||||::  :|| :||||||:|:|||||
Db        380 CRIWEMSKQWSERVCEEFYRQGELEQKFELEISPLCNQQKDSIPSIQIGFMSYIVEPLFR 439

Qy        371 EWARFS-NTRLSQTMLGHVGLNKASWKGLQREQSSSEDTDAA 411
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Db        440 EWAHFTGNSTLSENMLGHLAHNKAQWKSLLPRQHRSRGSSGS 481


RESULT 6
US-09-330-970-3
; Sequence 3, Application US/09330970
; Patent No. 6146876
; GENERAL INFORMATION:
;  APPLICANT: Robison, Keith E.
;  APPLICANT: Kapeller-Libermann, Rosana
;  APPLICANT: White, David
;  TITLE OF INVENTION: A No. 6146876el Human Cyclic Nucleotide
;  TITLE OF INVENTION: Phophodiesterase
;  FILE REFERENCE: 5800-28
;  CURRENT APPLICATION NUMBER: US/09/330,970
;  CURRENT FILING DATE: 1999-06-11
;  EARLIER APPLICATION NUMBER: 09/277,423
;  EARLIER FILING DATE: 1999-03-26
;  NUMBER OF SEQ ID NOS: 40
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 3
;    LENGTH: 320
;    TYPE: PRT
;    ORGANISM: Homo sapiens
US-09-330-970-3

  Query Match             38.8%;  Score 871;  DB 3;  Length 320;
  Best Local Similarity   66.9%;  Pred. No. 6.1e-85;
  Matches  160;  Conservative   34;  Mismatches   45;  Indels    0;  Gaps    0;

Qy         11 GDVRVRSRAGFESERRGSHPYIDFRIFHSQSEIEVSVSARNIRRLLSFQRYLRSSRFFRG 70
              ||:|:| : |  :|||||:|:||||: :| :      : : ::||||||||  :||  ||
Db         80 GDIRLRGQTGVRAERRGSYPFIDFRLLNSTTYSGEIGTKKKVKRLLSFQRYFHASRLLRG 139

Qy         71 TAVSNSLNILDDDYNGQAKCMLEKVGNWNFDIFLFDRLTNGNSLVSLTFHLFSLHGLIEY 130
                    |::||:|| |||: || ||| |:||||||||||||||:|  |||: |||| :
Db        140 IIPQAPLHLLDEDYLGQARHMLSKVGMWDFDIFLFDRLTNGNSLVTLLCHLFNTHGLIHH 199

Qy        131 FHLDMMKLRRFLVMIQEDYHSQNPYHNAVHAADVTQAMHCYLKEPKLANSVTPWDILLSL 190
              | |||: | |||||:|||||||||||||||||||||||||||||||: :|| ||:| |
Db        200 FKLDMVTLHRFLVMVQEDYHSQNPYHNAVHAADVTQAMHCYLKEPKLASFLTPLDIMLGL 259

Qy        191 IAAATHDLDHPGVNQPFLIKTNHYLATLYKNTSVLENHHWRSAVGLLRESGLFSHLPLE 249
              :||| ||:|||||||||||||:|| ||:| |||||||||| :|:|||| | :||| |
Db        260 LAAAAHDVDHPGVNQPFLIKTNHHLANLYQNMSVLENHHWRSTIGMLRESRLLAHLPKE 318


RESULT 7
US-08-974-565C-9
; Sequence 9, Application US/08974565C
; Patent No. 5932423
;  GENERAL INFORMATION:
;    APPLICANT:  Au-Young, Janice
;    APPLICANT:  Cocks, Benjamin G.
;    APPLICANT:  Coleman, Roger
;    APPLICANT:  Seilhamer, Jeffrey J.
;    APPLICANT:  Fisher, Douglas A.
;    TITLE OF INVENTION:  CYCLIC NUCLEOTIDE PHOSPHODIESTERASES
;    NUMBER OF SEQUENCES:  18
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Incyte Pharmaceuticals, Inc.
;      STREET:  3174 Porter Dr.
;      CITY:  Palo Alto
;      STATE:  CA
;      COUNTRY:  USA
;      ZIP:  94304
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ for Windows Version 2.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/974,565C
;      FILING DATE:  Herewith
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/624,663
;      FILING DATE:  March 25, 1996
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Murry, Lynn E.
;      REGISTRATION NUMBER:  42,918
;      REFERENCE/DOCKET NUMBER:  PF-0057-1 CIP
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  650-855-0555
;      TELEFAX:  650-845-4166
;  INFORMATION FOR SEQ ID NO:  9:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  610 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    IMMEDIATE SOURCE:
;      LIBRARY:  GenBank
;      CLONE:  1705952
US-08-974-565C-9

  Query Match             24.7%;  Score 555;  DB 2;  Length 610;
  Best Local Similarity   32.6%;  Pred. No. 1.5e-50;
  Matches  127;  Conservative   77;  Mismatches  154;  Indels   32;  Gaps    7;

Qy          8 RMLGDVRVRSRAGFESERRGSHPYIDFRIFHSQSEIEVSVSARNIRRLLSFQR----YLR 63
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Db         29 RELTHLSEMSRSGNQVSEYISNTFLD-----KQNEVEIPSPTPRQR---AFQQPPPSVLR 80

Qy         64 SSR------FFRGTAVSNSLNI------LDDDYNGQAKCMLEKVGNWNFDIFLFDRLTNG 111

Db         81 QSQPMSQITGLKKLVHTGSLNTNVPRFGVKTDQEDLLAQELENLSKWGLNIFCVSEYAGG 140

Qy        112 NSLVSLTFHLFSLHGLIEYFHLDMMKLRRFLVMIQEDYHSQNPYHNAVHAADVTQAMHCY 171

Db        141 RSLSCIMYTIFQERDLLKKFHIPVDTMMMYMLTLEDHYHADVAYHNSLHAADVLQSTHVL 200

Qy        172 LKEPKLANSVTPWDILLSLIAAATHDLDHPGVNQPFLIKTNHYLATLYKNTSVLENHHWR 231

Db        201 LATPALDAVFTDLEILAALFAAAIHDVDHPGVSNQFLINTNSELALMYNDESVLENHHLA 260

Qy        232 SAVGLLRESG--LFSHLPLESRQQMETQIGALILATDISRQNEYLSLFRSHLD------R 283

Db        261 VGFKLLQEENCDIFQNLSKRQRQSLRKMVIDMVLATDMSKHMTLLADLKTMVETKKVTSS 320

Qy        284 GDLCLEDTRHRHLVLQMALKCADICNPCRTWELSKQWSEKVTEEFFHQGDIEKKYHLGVS 343

Db        321 GVLLLDNYSDRIQVLRNMVHCADLSNPTKPLELYRQWTDRIMAEFFQQGDRERERGMEIS 380

Qy        344 PLCDRHTESIANIQIGFMTYLVEPLFTEWA 373

Db        381 PMCDKHTASVEKSQVGFIDYIVHPLWETWA 410


RESULT 8
US-09-255-748-9
; Sequence 9, Application US/09255748
; Patent No. 6080548
;  GENERAL INFORMATION:
;    APPLICANT:  Au-Young, Janice
;    APPLICANT:  Cocks, Benjamin G.
;    APPLICANT:  Coleman, Roger
;    APPLICANT:  Seilhamer, Jeffrey J.
;    APPLICANT:  Fisher, Douglas A.
;    TITLE OF INVENTION:  CYCLIC NUCLEOTIDE PHOSPHODIESTERASES
;    NUMBER OF SEQUENCES:  9
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Incyte Pharmaceuticals, Inc.
;      STREET:  3174 Porter Dr.
;      CITY:  Palo Alto
;      STATE:  CA
;      COUNTRY:  USA
;      ZIP:  94304
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ for Windows Version 2.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/255,748
;      FILING DATE:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/974,565
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Billings, Lucy J.
;      REGISTRATION NUMBER:  36,749
;      REFERENCE/DOCKET NUMBER:  PF-0057-1 CIP
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  650-855-0555
;      TELEFAX:  650-845-4166
;  INFORMATION FOR SEQ ID NO:  9:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  610 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    IMMEDIATE SOURCE:
;      LIBRARY:  GenBank
;      CLONE:  1705952
US-09-255-748-9

  Query Match           24.7%;  Score 555;  DB 3;  Length 610;
  Best Local Similarity  32.6%;  Pred. No. 1.5e-50;
  Matches  127;  Conservative   77;  Mismatches  154;  Indels   32;  Gaps    7;

Qy          8 RMLGDVRVRSRAGFESERRGSHPYIDFRIFHSQSEIEVSVSARNIRRLLSFQR----YLR 63

Db         29 RELTHLSEMSRSGNQVSEYISNTFLD-----KQNEVEIPSPTPRQR---AFQQPPPSVLR 80

Qy         64 SSR------FFRGTAVSNSLNI------LDDDYNGQAKCMLEKVGNWNFDIFLFDRLTNG 111

Db         81 QSQPMSQITGLKKLVHTGSLNTNVPRFGVKTDQEDLLAQELENLSKWGLNIFCVSEYAGG 140

Qy        112 NSLVSLTFHLFSLHGLIEYFHLDMMKLRRFLVMIQEDYHSQNPYHNAVHAADVTQAMHCY 171

Db        141 RSLSCIMYTIFQERDLLKKFHIPVDTMMMYMLTLEDHYHADVAYHNSLHAADVLQSTHVL 200

Qy        172 LKEPKLANSVTPWDILLSLIAAATHDLDHPGVNQPFLIKTNHYLATLYKNTSVLENHHWR 231

Db        201 LATPALDAVFTDLEILAALFAAAIHDVDHPGVSNQFLINTNSELALMYNDESVLENHHLA 260

Qy        232 SAVGLLRESG--LFSHLPLESRQQMETQIGALILATDISRQNEYLSLFRSHLD------R 283

Db        261 VGFKLLQEENCDIFQNLSKRQRQSLRKMVIDMVLATDMSKHMTLLADLKTMVETKKVTSS 320

Qy        284 GDLCLEDTRHRHLVLQMALKCADICNPCRTWELSKQWSEKVTEEFFHQGDIEKKYHLGVS 343

Db        321 GVLLLDNYSDRIQVLRNMVHCADLSNPTKPLELYRQWTDRIMAEFFQQGDRERERGMEIS 380

Qy        344 PLCDRHTESIANIQIGFMTYLVEPLFTEWA 373

Db        381 PMCDKHTASVEKSQVGFIDYIVHPLWETWA 410


RESULT 9
US-07-688-352C-4
; Sequence 4, Application US/07688352C
; Patent No. 5527896
;  GENERAL INFORMATION:
;    APPLICANT:  Wigler, Michael H.
;    APPLICANT:  Colicelli, John J.
;    TITLE OF INVENTION:  Cloning by Complementation and Related
;    TITLE OF INVENTION:  Processes
;    NUMBER OF SEQUENCES:  57
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Marshall, O'Toole, Gerstein, Murray &
;      ADDRESSEE:  Bicknell
;      STREET:  Two First National Plaza, 20 South Clark
;      STREET:  Street
;      CITY:  Chicago
;      STATE:  Illinois
;      COUNTRY:  USA
;      ZIP:  60603
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/07/688,352C
;      FILING DATE:  19910419
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/511,715
;      FILING DATE:  20-APR-1990
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Borun, Michael F.
;      REGISTRATION NUMBER:  25447
;      REFERENCE/DOCKET NUMBER:  27805/30197
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (312) 346-5750
```

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;      TELEFAX:  (312) 984-9740
;      TELEX:  25-3856
;  INFORMATION FOR SEQ ID NO:  4:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  562 amino acids
;      TYPE:  AMINO ACID
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-07-688-352C-4

  Query Match             24.5%;  Score 550;  DB 1;  Length 562;
  Best Local Similarity   31.8%;  Pred. No. 4.5e-50;
  Matches  122;  Conservative   84;  Mismatches  152;  Indels   26;  Gaps    6;

Qy          8 RMLGDVRVRSRAGFESERRGSHPYIDFRIFHSQSEIEVSVSARNIRR---------LLSF 58
              | |  :   ||:| :     |: ::|      |:::|:    :  |           :|
Db         82 RELTHLSEMSRSGNQVSEYISNTFLD-----KQNDVEIPSPTQKDREKKKKQQLMTQISG 136

Qy         59 QRYLRSSRFFRGTAVSN-SLNILDDDYNGQAKCMLEKVGNWNFDIFLFDRLTNGNSLVSL 117
               : |  |      |::|   :|  ::|:  :    || :  |  :||     ::   |  :
Db        137 VKKLMHSSSLNNTSISRFGVNTENEDHLAKE---LEDLNKWGLNIFNVAGYSHNRPLTCI 193

Qy        118 TFHLFSLHGLIEYFHLDMMKLRRFLVMIQEDYHSQNPYHNAVHAADVTQAMHCYLKEPKL 177
               : :|     |:: | :       ::: ::: |||   |||::|||| |: |  |  | |
Db        194 MYAIFQERDLLKTFKISSDTFVTYMMTLEDHYHSDVAYHNSLHAADVAQSTHVLLSTPAL 253

Qy        178 ANSVTPWDILLSLIAAATHDLDHPGVNQPFLIKTNHYLATLYKNTSVLENHHWRSAVGLL 237
                 |  :|| :: ||| ||:|||||:  ||| ||  || :| : |||||||      ||
Db        254 DAVFTDLEILAAIFAAAIHDVDHPGVSNQFLINTNSELALMYNDESVLENHHLAVGFKLL 313

Qy        238 RES--GLFSHLPLESRQQMETQIGALILATDISRQNEYLSLFRSHLD------RGDLCLE 289
               :|    :| :|  : || :   :  ::||||:|:    |:  :: ::       | | |:
Db        314 QEEHCDIFQNLTKKQRQTLRKMVIDMVLATDMSKHMSLLADLKTMVETKKVTSSGVLLLD 373

Qy        290 DTRHRHLVLQMALKCADICNPCRTWELSKQWSEKVTEEFFHQGDIEKKYHLGVSPLCDRH 349
               :   |  ||:  : |||: || :: || :|||:::: |||| ||| |::  : :||:||:|
Db        374 NYTDRIQVLRNMVHCADLSNPTKSLELYRQWTDRIMEEFFQQGDKERERGMEISPMCDKH 433

Qy        350 TESIANIQIGFMTYLVEPLFTEWA 373
               | |:   |:||: |:| ||:  ||
Db        434 TASVEKSQVGFIDYIVHPLWETWA 457


RESULT 10
US-08-942-521B-8
; Sequence 8, Application US/08942521B
; Patent No. 5932477
;  GENERAL INFORMATION:
;    APPLICANT:  Livi, George P.
;    APPLICANT:  McLaughlin, Megan M.
;    APPLICANT:  Torphy, Theodore J.
;    TITLE OF INVENTION:  Human Brain Phosphodiesterase
;    NUMBER OF SEQUENCES:  9
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  SmithKline Beecham Corporation
;      STREET:  Corporate Patents/ P.O.Box 1539
;      CITY:  King of Prussia
;      STATE:  PA
;      COUNTRY:  USA
;      ZIP:  19406-0939
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/942,521B
;      FILING DATE:  October 2, 1997
;      CLASSIFICATION:  536
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/446,386
;      FILING DATE:  22 May 1995
;      CLASSIFICATION:  536
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/029,334
;      FILING DATE:  10 March 1993
;      CLASSIFICATION:  536
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Elizabeth J. Hecht
;      REGISTRATION NUMBER:  41,824
;      REFERENCE/DOCKET NUMBER:  P50145C1FWC
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (215) 270-5009
;      TELEFAX:  (215) 270-5090
;  INFORMATION FOR SEQ ID NO:  8:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  562 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-942-521B-8

  Query Match             24.5%;  Score 550;  DB 2;  Length 562;
  Best Local Similarity   31.8%;  Pred. No. 4.5e-50;
  Matches  122;  Conservative   84;  Mismatches  152;  Indels   26;  Gaps    6;

Qy          8 RMLGDVRVRSRAGFESERRGSHPYIDFRIFHSQSEIEVSVSARNIRR---------LLSF 58
              | |  :   ||:| :     |: ::|      |:::|:    :  |           :|
Db         82 RELTHLSEMSRSGNQVSEYISNTFLD-----KQNDVEIPSPTQKDREKKKKQQLMTQISG 136

Qy         59 QRYLRSSRFFRGTAVSN-SLNILDDDYNGQAKCMLEKVGNWNFDIFLFDRLTNGNSLVSL 117
               : |  |      |::|   :|  ::|:  :    || :  |  :||     ::   |  :
Db        137 VKKLMHSSSLNNTSISRFGVNTENEDHLAKE---LEDLNKWGLNIFNVAGYSHNRPLTCI 193

Qy        118 TFHLFSLHGLIEYFHLDMMKLRRFLVMIQEDYHSQNPYHNAVHAADVTQAMHCYLKEPKL 177
               : :|     |:: | :       ::: ::: |||   |||::|||| |: |  |  | |
Db        194 MYAIFQERDLLKTFKISSDTFVTYMMTLEDHYHSDVAYHNSLHAADVAQSTHVLLSTPAL 253

Qy        178 ANSVTPWDILLSLIAAATHDLDHPGVNQPFLIKTNHYLATLYKNTSVLENHHWRSAVGLL 237
                 |  :|| :: ||| ||:|||||:  ||| ||  || :| : |||||||      ||
Db        254 DAVFTDLEILAAIFAAAIHDVDHPGVSNQFLINTNSELALMYNDESVLENHHLAVGFKLL 313

Qy        238 RES--GLFSHLPLESRQQMETQIGALILATDISRQNEYLSLFRSHLD------RGDLCLE 289
               :|    :| :|  : || :   :  ::||||:|:    |:  :: ::       | | |:
Db        314 QEEHCDIFQNLTKKQRQTLRKMVIDMVLATDMSKHMSLLADLKTMVETKKVTSSGVLLLD 373

Qy        290 DTRHRHLVLQMALKCADICNPCRTWELSKQWSEKVTEEFFHQGDIEKKYHLGVSPLCDRH 349
               :   |  ||:  : |||: || :: || :||:::: |||| ||| |::  : :||:||:|
Db        374 NYTDRIQVLRNMVHCADLSNPTKSLELYRQWTDRIMEEFFQQGDKERERGMEISPMCDKH 433

Qy        350 TESIANIQIGFMTYLVEPLFTEWA 373
               | |:   |:||: |:| ||:  ||
Db        434 TASVEKSQVGFIDYIVHPLWETWA 457


RESULT 11
US-08-474-379C-4
; Sequence 4, Application US/08474379C
; Patent No. 5977305
;  GENERAL INFORMATION:
;    APPLICANT:  Wigler, Michael H.
;    APPLICANT:  Colicelli, John J.
;    TITLE OF INVENTION:  CLONING BY COMPLEMENTATION AND RELATED
;    TITLE OF INVENTION:  PROCESSES
;    NUMBER OF SEQUENCES:  88
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Marshall, O'Toole, Gerstein, Murray & Borun
;      STREET:  233 South Wacker Drive/6300 Sears Tower
;      CITY:  Chicago
;      STATE:  Illinois
;      COUNTRY:  United States of America
;      ZIP:  60606-6402
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
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;       SOFTWARE:  PatentIn Release #1.0, Version #1.30
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/474,379C
;       FILING DATE:  07-JUN-1995
;       CLASSIFICATION:  435
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  US 07/511,715
;       FILING DATE:  20-APR-1990
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  US 08/206,188
;       FILING DATE:  01-MAR-1994
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  US 07/688,352
;       FILING DATE:  19-APR-1991
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Clough, David W.
;       REGISTRATION NUMBER:  36,107
;       REFERENCE/DOCKET NUMBER:  27866/32771
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  (312) 474-6300
;       TELEFAX:  (312) 474-0448
;   INFORMATION FOR SEQ ID NO:  4:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  562 amino acids
;       TYPE:  amino acid
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  protein
US-08-474-379C-4

  Query Match             24.5%;  Score 550;  DB 2;  Length 562;
  Best Local Similarity   31.8%;  Pred. No. 4.5e-50;
  Matches  122;  Conservative   84;  Mismatches  152;  Indels   26;  Gaps    6;

Qy          8 RMLGDVRVRSRAGFESERRGSHPYIDFRIFHSQSEIEVSVSARNIRR---------LLSF 58
              | |  :   ||:| :      |: ::|      |:::|:    :  |           :|
Db         82 RELTHLSEMSRSGNQVSEYISNTFLD-----KQNDVEIPSPTQKDREKKKKQQLMTQISG 136

Qy         59 QRYLRSSRFFRGTAVSN-SLNILDDDYNGQAKCMLEKVGNWNFDIFLFDRLTNGNSLVSL 117
              : |  |      |::|   :|  ::|:  :    || :  |  :||     ::   |  :
Db        137 VKKLMHSSSLNNTSISRFGVNTENEDHLAKE---LEDLNKWGLNIFNVAGYSHNRPLTCI 193

Qy        118 TFHLFSLHGLIEYFHLDMMKLRRFLVMIQEDYHSQNPYHNAVHAADVTQAMHCYLKEPKL 177
               : :|    |:: | :        ::: ::: |||   |||::||||| |: |  |  | |
Db        194 MYAIFQERDLLKTFKISSDTFVTYMMTLEDHYHSDVAYHNSLHAADVAQSTHVLLSTPAL 253

Qy        178 ANSVTPWDILLSLIAAATHDLDHPGVNQPFLIKTNHYLATLYKNTSVLENHHWRSAVGLL 237
              |  :|| :: ||| ||:|||||:  ||| ||  || :| : |||||||       ||
Db        254 DAVFTDLEILAAIFAAAIHDVDHPGVSNQFLINTNSELALMYNDESVLENHHLAVGFKLL 313

Qy        238 RES--GLFSHLPLESRQQMETQIGALILATDISRQNEYLSLFRSHLD------RGDLCLE 289
              :|    :| :|  : || :   :  ::||||:|:     |: :: ::       | | |:
Db        314 QEEHCDIFQNLTKKQRQTLRKMVIDMVLATDMSKHMSLLADLKTMVETKKVTSSGVLLLD 373

Qy        290 DTRHRHLVLQMALKCADICNPCRTWELSKQWSEKVTEEFFHQGDIEKKYHLGVSPLCDRH 349
              :  |  ||:  : |||: || :: || :||:::: |||| ||| |::  : :||:||:|
Db        374 NYTDRIQVLRNMVHCADLSNPTKSLELYRQWTDRIMEEFFQQGDKERERGMEISPMCDKH 433

Qy        350 TESIANIQIGFMTYLVEPLFTEWA 373
              | |:   |:||: |:| ||:  ||
Db        434 TASVEKSQVGFIDYIVHPLWETWA 457


RESULT 12
US-09-146-249A-4
; Sequence 4, Application US/09146249A
; Patent No. 6069240
;  GENERAL INFORMATION:
;    APPLICANT:  Wigler, Michael H.
;    APPLICANT:  Colicelli, John J.
;    TITLE OF INVENTION:  Cloning by Complementation and Related
;    TITLE OF INVENTION:  Processes
;    NUMBER OF SEQUENCES:  85
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Marshall, O'Toole, Gerstein, Murray & Borun
;      STREET:  6300 Sears Tower, 233 South Wacker Drive
;      CITY:  Chicago
;      STATE:  Illinois
;      COUNTRY:  United States of America
;      ZIP:  60606-6402
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/146,249A
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/511,715
;      FILING DATE:  20-APR-1990
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Clough, David W.
;      REGISTRATION NUMBER:  36,107
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  312/474-6300
;      TELEFAX:  312-474-0448
;      TELEX:  25-3856
;  INFORMATION FOR SEQ ID NO:  4:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  562 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-09-146-249A-4

  Query Match             24.5%;  Score 550;  DB 3;  Length 562;
  Best Local Similarity   31.8%;  Pred. No. 4.5e-50;
  Matches  122;  Conservative   84;  Mismatches  152;  Indels   26;  Gaps    6;

Qy          8 RMLGDVRVRSRAGFESERRGSHPYIDFRIFHSQSEIEVSVSARNIRR---------LLSF 58
              | |  :   ||:| :      |: ::|      |:::|:    :  |           :|
Db         82 RELTHLSEMSRSGNQVSEYISNTFLD-----KQNDVEIPSPTQKDREKKKKQQLMTQISG 136

Qy         59 QRYLRSSRFFRGTAVSN-SLNILDDDYNGQAKCMLEKVGNWNFDIFLFDRLTNGNSLVSL 117
              : |  |      |::|   :|  ::|:  :    || :  |  :||     ::   |  :
Db        137 VKKLMHSSSLNNTSISRFGVNTENEDHLAKE---LEDLNKWGLNIFNVAGYSHNRPLTCI 193

Qy        118 TFHLFSLHGLIEYFHLDMMKLRRFLVMIQEDYHSQNPYHNAVHAADVTQAMHCYLKEPKL 177
               : :|    |:: | :        ::: ::: |||   |||::||||| |: |  |  | |
Db        194 MYAIFQERDLLKTFKISSDTFVTYMMTLEDHYHSDVAYHNSLHAADVAQSTHVLLSTPAL 253

Qy        178 ANSVTPWDILLSLIAAATHDLDHPGVNQPFLIKTNHYLATLYKNTSVLENHHWRSAVGLL 237
              |  :|| :: ||| ||:|||||:  ||| ||  || :| : |||||||       ||
Db        254 DAVFTDLEILAAIFAAAIHDVDHPGVSNQFLINTNSELALMYNDESVLENHHLAVGFKLL 313

Qy        238 RES--GLFSHLPLESRQQMETQIGALILATDISRQNEYLSLFRSHLD------RGDLCLE 289
              :|    :| :|  : || :   :  ::||||:|:     |: :: ::       | | |:
Db        314 QEEHCDIFQNLTKKQRQTLRKMVIDMVLATDMSKHMSLLADLKTMVETKKVTSSGVLLLD 373

Qy        290 DTRHRHLVLQMALKCADICNPCRTWELSKQWSEKVTEEFFHQGDIEKKYHLGVSPLCDRH 349
              :  |  ||:  : |||: || :: || :||:::: |||| ||| |::  : :||:||:|
Db        374 NYTDRIQVLRNMVHCADLSNPTKSLELYRQWTDRIMEEFFQQGDKERERGMEISPMCDKH 433

Qy        350 TESIANIQIGFMTYLVEPLFTEWA 373
              | |:   |:||: |:| ||:  ||
Db        434 TASVEKSQVGFIDYIVHPLWETWA 457


RESULT 13
US-08-206-188B-4
; Sequence 4, Application US/08206188B
; Patent No. 6100025
;  GENERAL INFORMATION:
;    APPLICANT:  Wigler, Michael H.
;    APPLICANT:  Colicelli, John J.
```

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;    TITLE OF INVENTION:  Cloning by Complementation and Related
;    TITLE OF INVENTION:  Processes
;    NUMBER OF SEQUENCES:  84
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Marshall, O'Toole, Gerstein, Murray & Borun
;      STREET:  6300 Sears Tower, 233 South Wacker Drive
;      CITY:  Chicago
;      STATE:  Illinois
;      COUNTRY:  United States of America
;      ZIP:  60606-6402
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/206,188B
;      FILING DATE:  01-MAR-1994
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/511,715
;      FILING DATE:  20-APR-1990
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Clough, David W.
;      REGISTRATION NUMBER:  36107
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  312/474-6300
;      TELEFAX:  312-474-0448
;      TELEX:  25-3856
;  INFORMATION FOR SEQ ID NO:  4:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  562 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-206-188B-4

  Query Match             24.5%;  Score 550;  DB 3;  Length 562;
  Best Local Similarity   31.8%;  Pred. No. 4.5e-50;
  Matches  122;  Conservative   84;  Mismatches  152;  Indels   26;  Gaps    6;

Qy          8 RMLGDVRVRSRAGFESERRGSHPYIDFRIFHSQSEIEVSVSARNIRR---------LLSF 58
              | | :   ||:| :     |: ::|     |:::|:    :  |            :|
Db         82 RELTHLSEMSRSGNQVSEYISNTFLD-----KQNDVEIPSPTQKDREKKKKQQLMTQISG 136

Qy         59 QRYLRSSRFFRGTAVSN-SLNILDDDYNGQAKCMLEKVGNWNFDIFLFDRLTNGNSLVSL 117
               : |  |      |::|   :|  ::|:  :    || :  |  :||     ::   |  :
Db        137 VKKLMHSSSLNNTSISRFGVNTENEDHLAKE---LEDLNKWGLNIFNVAGYSHNRPLTCI 193

Qy        118 TFHLFSLHGLIEYFHLDMMKLRRFLVMIQEDYHSQNPYHNAVHAADVTQAMHCYLKEPKL 177
               : :|    |:: | :       ::: ::: |||   |||::|||| |: |  |  | |
Db        194 MYAIFQERDLLKTFKISSDTFVTYMMTLEDHYHSDVAYHNSLHAADVAQSTHVLLSTPAL 253

Qy        178 ANSVTPWDILLSLIAAATHDLDHPGVNQPFLIKTNHYLATLYKNTSVLENHHWRSAVGLL 237
                 |  :|| :: ||| ||:|||||:  ||| ||  || :| : |||||||      ||
Db        254 DAVFTDLEILAAIFAAAIHDVDHPGVSNQFLINTNSELALMYNDESVLENHHLAVGFKLL 313

Qy        238 RES--GLFSHLPLESRQQMETQIGALILATDISRQNEYLSLFRSHLD------RGDLCLE 289
              :|    :| :|  : || :   :  ::||||:|:    |:  :: ::       | | |:
Db        314 QEEHCDIFQNLTKKQRQTLRKMVIDMVLATDMSKHMSLLADLKTMVETKKVTSSGVLLLD 373

Qy        290 DTRHRHLVLQMALKCADICNPCRTWELSKQWSEKVTEEFFHQGDIEKKYHLGVSPLCDRH 349
              :   |  ||:  : |||: || :: || :||:::: |||| ||| |::  : :||:||:|
Db        374 NYTDRIQVLRNMVHCADLSNPTKSLELYRQWTDRIMEEFFQQGDKERERGMEISPMCDKH 433

Qy        350 TESIANIQIGFMTYLVEPLFTEWA 373
              | |:   |:||: |:| ||:  ||
Db        434 TASVEKSQVGFIDYIVHPLWETWA 457


RESULT 14
PCT-US91-02714-4
; Sequence 4, Application PC/TUS9102714
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;  GENERAL INFORMATION:
;    APPLICANT:  Wigler, Michael H.
;    APPLICANT:  Colicelli, John J.
;    TITLE OF INVENTION:  Cloning by Complementation and Related
;    TITLE OF INVENTION:  Processes
;    NUMBER OF SEQUENCES:  55
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Marshall, O'Toole, Gerstein, Murray &
;      ADDRESSEE:  Bicknell
;      STREET:  Two First National Plaza, 20 South Clark
;      STREET:  Street
;      CITY:  Chicago
;      STATE:  Illinois
;      COUNTRY:  USA
;      ZIP:  60603
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US91/02714
;      FILING DATE:  19910419
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 07/511,715
;      FILING DATE:  20-APR-1990
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Borun, Michael F.
;      REGISTRATION NUMBER:  25447
;      REFERENCE/DOCKET NUMBER:  27805/30197
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (312) 346-5750
;      TELEFAX:  (312) 984-9740
;      TELEX:  25-3856
;  INFORMATION FOR SEQ ID NO:  4:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  562 amino acids
;      TYPE:  AMINO ACID
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
PCT-US91-02714-4

  Query Match             24.5%;  Score 550;  DB 5;  Length 562;
  Best Local Similarity   31.8%;  Pred. No. 4.5e-50;
  Matches  122;  Conservative   84;  Mismatches  152;  Indels   26;  Gaps    6;

Qy          8 RMLGDVRVRSRAGFESERRGSHPYIDFRIFHSQSEIEVSVSARNIRR---------LLSF 58
              | | :   ||:| :     |: ::|     |:::|:    :  |            :|
Db         82 RELTHLSEMSRSGNQVSEYISNTFLD-----KQNDVEIPSPTQKDREKKKKQQLMTQISG 136

Qy         59 QRYLRSSRFFRGTAVSN-SLNILDDDYNGQAKCMLEKVGNWNFDIFLFDRLTNGNSLVSL 117
               : |  |      |::|   :|  ::|:  :    || :  |  :||     ::   |  :
Db        137 VKKLMHSSSLNNTSISRFGVNTENEDHLAKE---LEDLNKWGLNIFNVAGYSHNRPLTCI 193

Qy        118 TFHLFSLHGLIEYFHLDMMKLRRFLVMIQEDYHSQNPYHNAVHAADVTQAMHCYLKEPKL 177
               : :|    |:: | :       ::: ::: |||   |||::|||| |: |  |  | |
Db        194 MYAIFQERDLLKTFKISSDTFVTYMMTLEDHYHSDVAYHNSLHAADVAQSTHVLLSTPAL 253

Qy        178 ANSVTPWDILLSLIAAATHDLDHPGVNQPFLIKTNHYLATLYKNTSVLENHHWRSAVGLL 237
                 |  :|| :: ||| ||:|||||:  ||| ||  || :| : |||||||      ||
Db        254 DAVFTDLEILAAIFAAAIHDVDHPGVSNQFLINTNSELALMYNDESVLENHHLAVGFKLL 313

Qy        238 RES--GLFSHLPLESRQQMETQIGALILATDISRQNEYLSLFRSHLD------RGDLCLE 289
              :|    :| :|  : || :   :  ::||||:|:    |:  :: ::       | | |:
Db        314 QEEHCDIFQNLTKKQRQTLRKMVIDMVLATDMSKHMSLLADLKTMVETKKVTSSGVLLLD 373

Qy        290 DTRHRHLVLQMALKCADICNPCRTWELSKQWSEKVTEEFFHQGDIEKKYHLGVSPLCDRH 349
              :   |  ||:  : |||: || :: || :||:::: |||| ||| |::  : :||:||:|
Db        374 NYTDRIQVLRNMVHCADLSNPTKSLELYRQWTDRIMEEFFQQGDKERERGMEISPMCDKH 433

Qy        350 TESIANIQIGFMTYLVEPLFTEWA 373
              | |:   |:||: |:| ||:  ||
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Db        434 TASVEKSQVGFIDYIVHPLWETWA 457


RESULT 15
US-08-942-521B-2
; Sequence 2, Application US/08942521B
; Patent No. 5932477
;  GENERAL INFORMATION:
;    APPLICANT:  Livi, George P.
;    APPLICANT:  McLaughlin, Megan M.
;    APPLICANT:  Torphy, Theodore J.
;    TITLE OF INVENTION:  Human Brain Phosphodiesterase
;    NUMBER OF SEQUENCES:  9
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  SmithKline Beecham Corporation
;      STREET:  Corporate Patents/ P.O.Box 1539
;      CITY:  King of Prussia
;      STATE:  PA
;      COUNTRY:  USA
;      ZIP:  19406-0939
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/942,521B
;      FILING DATE:  October 2, 1997
;      CLASSIFICATION:  536
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/446,386
;      FILING DATE:  22 May 1995
;      CLASSIFICATION:  536
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/029,334
;      FILING DATE:  10 March 1993
;      CLASSIFICATION:  536
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Elizabeth J. Hecht
;      REGISTRATION NUMBER:  41,824
;      REFERENCE/DOCKET NUMBER:  P50145C1FWC
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (215) 270-5009
;      TELEFAX:  (215) 270-5090
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  564 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  protein
US-08-942-521B-2

  Query Match             24.5%;  Score 550;  DB 2;  Length 564;
  Best Local Similarity   31.8%;  Pred. No. 4.6e-50;
  Matches  122;  Conservative   84;  Mismatches  152;  Indels   26;  Gaps    6;

Qy          8 RMLGDVRVRSRAGFESERRGSHPYIDFRIFHSQSEIEVSVSARNIRR---------LLSF 58
              | |  :   ||:| :      |: ::|       |:::|:    :  |           :|
Db         84 RELTHLSEMSRSGNQVSEYISNTFLD-----KQNDVEIPSPTQKDREKKKKQQLMTQISG 138

Qy         59 QRYLRSSRFFRGTAVSN-SLNILDDDYNGQAKCMLEKVGNWNFDIFLFDRLTNGNSLVSL 117
               : |  |      |::|   :|  ::|:  :    || :  |  :||     ::   |  :
Db        139 VKKLMHSSSLNNTSISRFGVNTENEDHLAKE---LEDLNKWGLNIFNVAGYSHNRPLTCI 195

Qy        118 TFHLFSLHGLIEYFHLDMMKLRRFLVMIQEDYHSQNPYHNAVHAADVTQAMHCYLKEPKL 177
                : :|    |:: | :       ::: ::: |||   |||::|||| |: |  |  | |
Db        196 MYAIFQERDLLKTFRISSDTFITYMMTLEDHYHSDVAYHNSLHAADVAQSTHVLLSTPAL 255

Qy        178 ANSVTPWDILLSLIAAATHDLDHPGVNQPFLIKTNHYLATLYKNTSVLENHHWRSAVGLL 237
                |  :|| :: ||| ||:|||||:  ||| ||  || :| : |||||||      ||
Db        256 DAVFTDLEILAAIFAAAIHDVDHPGVSNQFLINTNSELALMYNDESVLENHHLAVGFKLL 315

Qy        238 RES--GLFSHLPLESRQQMETQIGALILATDISRQNEYLSLFRSHLD------RGDLCLE 289
                :|    :| :|  : || :   :  ::||||:|:    |:  :: ::       | | |:
Db        316 QEEHCDIFMNLTKKQRQTLRKMVIDMVLATDMSKHMSLLADLKTMVETKKVTSSGVLLLD 375

Qy        290 DTRHRHLVLQMALKCADICNPCRTWELSKQWSEKVTEEFFHQGDIEKKYHLGVSPLCDRH 349
                :   |  ||:  : |||: || :: || :||:::: |||| ||| |::  : :||:||:|
Db        376 NYTDRIQVLRNMVHCADLSNPTKSLELYRQWTDRIMEEFFQQGDKERERGMEISPMCDKH 435

Qy        350 TESIANIQIGFMTYLVEPLFTEWA 373
                | |:   |:||: |:| ||:  ||
Db        436 TASVEKSQVGFIDYIVHPLWETWA 459


Search completed: May 26, 2004, 09:29:02
Job time : 24 secs
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            GapLengthWeight: 2

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 Name: us-09-966-781a-3  Len:   426  Check: 9989  Weight:  1.00
 Name: us-09-966-781a-1  Len:   426  Check: 3571  Weight:  1.00

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us-09-966-781a-3  DQTALYIRML GDVRVRSRAG FETERRGSHP YIDFRIFHAQ SEIEASVSAR
us-09-966-781a-1  DQTALYIRML GDVRVRSRAG FESERRGSHP YIDFRIFHSQ SEIEVSVSAR

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us-09-966-781a-3  NIRRLLSFQR YLRSSRFFRG ATVCRSLNIL DEDYNGQAKC MLEKVGNWNF
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                  101                                                 150
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us-09-966-781a-3  DIFLFDRLTN GNSLVSLTFH LFSLHGLIEY FHLDMVKLRR FLVMIQEDYH
us-09-966-781a-1  DIFLFDRLTN GNSLVSLTFH LFSLHGLIEY FHLDMMKLRR FLVMIQEDYH

                  151                                                 200
us-09-966-781a-2  SQNPYHNAVH AADVTQAMHC YLKEPKLASS VTPWDILLSL IAAATHDLDH
us-09-966-781a-3  SQNPYHNAVH AADVTQAMHC YLKEPKLANS VTPWDILLSL IAAATHDLDH
us-09-966-781a-1  SQNPYHNAVH AADVTQAMHC YLKEPKLANS VTPWDILLSL IAAATHDLDH

                  201                                                 250
us-09-966-781a-2  PGVNQPFLIK TNHYLATLYK NSSVLENHHW RSAVGLLRES GLFSHLPLES
us-09-966-781a-3  PGVNQPFLIK TNHYLATLYK NTSVLENHHW RSAVGLLRES GLFSHLPLES
us-09-966-781a-1  PGVNQPFLIK TNHYLATLYK NTSVLENHHW RSAVGLLRES GLFSHLPLES

                  251                                                 300
us-09-966-781a-2  RQEMEAQIGA LILATDISRQ NEYLSLFRSH LDKGDLHLDD GRHRHLVLQM
us-09-966-781a-3  RHEMEAQIGA LILATDISRQ NEYLSLFRSH LDKGDLHLDD GRHRHLVLQM
us-09-966-781a-1  RQQMETQIGA LILATDISRQ NEYLSLFRSH LDRGDLCLED TRHRHLVLQM

                  301                                                 350
us-09-966-781a-2  ALKCADICNP CRNWELSKQW SEKVTEEFFH QGDIEKKYHL GVSPLCDRQT
us-09-966-781a-3  ALKCADICNP CRNWELSKQW SEKVTEEFFH QGDIEKKYHL GVSPLCDRQT
us-09-966-781a-1  ALKCADICNP CRTWELSKQW SEKVTEEFFH QGDIEKKYHL GVSPLCDRHT

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us-09-966-781a-2  ESIANIQIGF MTYLVEPLFT EWARFSATRL SQTMLGHVGL NKASWKGLQR
us-09-966-781a-3  ESIANIQIGF MTYLQEPLFT EWARFSDTRL SQTMLGHVGL NKASWKGLQR
us-09-966-781a-1  ESIANIQIGF MTYLVEPLFT EWARFSNTRL SQTMLGHVGL NKASWKGLQR

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us-09-966-781a-2  QQPSSEDANA AFELNSQLLT QENRLS
us-09-966-781a-3  QQPSSEDASA AFELNSQLLT QENRLS
us-09-966-781a-1  EQSSSEDTDA AFELNSQLLP QENRLS
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